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KUBO *et al.* Appl. No. 09/665,510

Remarks

No new matter has been added. The specification has been amended to direct the entry of this sequence listing after the claims of the above identified application, to provide the SEQ ID NOs next to the specific sequences, to correct paragraph formatting, and to correct obvious typographical errors. The tables on pages 103-116 have been reformatted so that the sequence identifiers could be added to the tables while maintaining the proper page margins.

In accordance with 37 C.F.R. § 1.821(g), this submission includes no new matter.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above application are the same.

It is respectfully believed that this application is now in condition for examination.

Early notice to this effect is respectfully requested.

Respectfully submitted,

Valenellailson

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In the Specification:

A sequence listing was added.

Please replace the paragraph beginning on page 1, line 2 with the following paragraph:

The present application is a continuation in part of 08/347,610, filed December 1, 1994, which is a continuation in part of U.S. Patent Application Ser. No. 08/159,339, filed Nov. 29, 1993, now U.S. Patent 6,037,135, which is a continuation in part of U.S. Patent Application Ser. No. 08/103,396, filed Aug. 6, 1993 (now abandoned), which is a continuation in part of U.S. Patent Application Ser. No. 08/027,746, filed Mar. 5, 1993 (now abandoned), which is a continuation in part of U.S. Patent Application Ser. No. 07/926,666, filed Aug. 7, 1992 (now abandoned). The present application is also related to U.S. Patent Application Ser. No. 08/186,266, filed January 25, 1994, now U.S. Patent 5,662,907, which is a continuation in part of U.S. Patent Application Ser. No. 08/159,339 as described above. All of the above applications and patents are hereby incorporated by reference as if fully set forth.

The paragraph beginning on page 55, line 12 was replaced with the following paragraph:

As a radiolabeled probe, the peptide 941.12 (KVFPYALINK) (SEQ ID NO:52), containing an A3.2 motif, was used. This peptide contains the anchor residues V_2 and K_{10} ,

associated with A3.2-specific binders, described above. A Y residue was inserted at position 5 to allow for <u>radioiodination</u> radiolodination. Peptides were labeled by the use of the Chloramine T method, Buus et al., <u>Science</u> 235:1352 (1987), which is incorporated herein by reference.

The paragraph beginning on page 57, line 11 was replaced with the following paragraph:

The cell line BVR was used as a source of HLA. The dependency of the binding on MHC concentration in presence or absence of β_2 M are shown in Fig. 6, while Fig. 7 depicts the dose dependency of the inhibition by excess unlabeled ligand. Finally, Fig. 8 shows a Scatchard analysis experiment. Values of apparent kD of -6 nM and of 10% active receptor were obtained, and were remarkable for their similarity to the values obtained for A2.1 and A3.2. The sequence of the peptide used as a radiolabeled probe (940-06) is AVDLYHFLK (SEQ ID NO:53).

The paragraph beginning on page 57, line 22 was replaced with the following paragraph:

In this case, the EBV cell line Steinlin was used as a source of purified HLA. The same protocol previously applied to purification of other HLA alleles (i.e., depletion of B, C molecules by a B1.23.2 mAb column, followed by purification of A molecules by means of a W632 mAb column) was utilized. On the basis of the pool sequencing data, consensus peptides were synthesized, directly radiolabeled, and tested for HLA binding using the standard protocol (1 mM β_2 M, 2 days RT incubation in presence of protease inhibitors). A

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graph illustrating the relationship between % binding and μ M input HLA A1 is shown in Fig. 9. From the data, it was concluded that in analogy with what was observed for HLA A2, 3, and 11, as little as 30 nM are sufficient to obtain ~10% binding. The sequence of the peptide used as a radiolabeled probe (944.02) is YLEPAIAKY (SEO ID NO:54). In the next set of experiments, the specificity of the assay established was verified by its inhabitability inhibitability by excess unlabeled peptide. The IC50% was measured (Fig. 10) as \simeq ~20 nM. Further Scatchard analysis (Fig. 11) verified that the apparent K_D of the interaction corresponded to 21 nM, with a % of active receptor corresponding to 5.1%.

The paragraph beginning on page 58, line 6 was replaced with the following paragraph:

HLA A24 molecules were purified from the KT3 EBV cell line. In this case, two consensus peptides whose sequences were based on the pool sequencing data have been synthesized. Their sequences are: 979-01, AYIDNVYKF (SEQ ID NO:55) and 979.02, AYIDNYNKF (SEQ ID NO:56). The results of experiments in which the % bound of these two peptides as a function of input MHC was measured are shown in Fig. 12. In both cases, 10-15% binding was obtained with as little as 20-50 nM MHC. Cold inhibition experiments (Fig. 13), limiting MHC concentrations, revealed that the binding was readily inhibitable by excess unlabeled peptide, with an apparent K_D of 30 and 60 nM, respectively. Further Scatchard experiments verified values of 136 nM and 28 nM, respectively. The apparent % of available receptor (active MHC) were 8.3% and 7.4%, respectively (Fig. 9a and b). On the basis of these data, peptide 979.02 was arbitrarily selected as standard label indicator for A24 assays. Furthermore, on the basis of the data herein described, we also conclude

that the goal of establishing an A24-specific binding assay has been accomplished. In conclusion, specific assays for the five major HLA alleles have been described.

The paragraph beginning on page 59, line 5 was replaced with the following paragraph:

For example, in the case of A3.2, a motif has been defined with a hydrophobic residue in position 2 and a positive charge (K) in position 9. Thus, to verify that the presence of these two anchor residues would allow, in the context of a poly A backbone, for A3.2 binding, the poly A analog with the sequence AMAAAAAK (SEQ ID NO:61) was synthesized (Table 13).

The paragraph beginning of page 65, line 30 was replaced with the following paragraph:

Table 20(b) describes the peptides that bound to HLA-A3.2 molecules. Seven peptides were identified as high affinity binders, 6 as intermediate affinity binders and 13 as low affinity binders. Table 20(c) describes the peptides that bound to HLA-A11.2 molecules. Six high affinity peptides were identified, 4 intermediate affinity binders and 10 low affinity binders. Two high affinity binding peptides (E6-59 IVYRDGNPY (SEQ ID NO:142) and E6-80 ISEYRHYAY (SEQ ID NO:132)) and two weak affinity binding peptides with a Y at the 9th position (E6-42 QQLLRREVY (SEQ ID NO:155), E6-69 VADKALKFY (SEQ ID NO:133)) were identified for HLA-A11.2. Considering the high binding strength of the first two peptides and the similarity between the HLA-A11.2 motif and the HLA-A3.2 motif in which Y's are preferred at the 9th aa position, tyrosines should

be included at the 9th position in the HLA-A11.2 motif. Comparing Tables 21(b) and (c) it is clear that there is a large overlap of peptides that bound to both A3.2 and A11.2 molecules. Eighteen out of 28 E6 and E7 peptides binding to these two HLA molecules overlapped and only 8 peptides were unique for HLA-A3.2 and 2 peptides unique for HLA-A11.2.

The paragraph beginning on page 66, line 11 was replaced with the following paragraph:

Finally, Table 20(d) describes the peptides that bound to HLA-A24 molecules. Here 2 peptides were identified as high affinity binding peptides, 5 as intermediate affinity binding peptides and 5 as low binding peptides. One high affinity peptide (E6-72 KALKFYSKI) (SEQ_ID_NO:168) and one intermediate affinity peptide (E7-49 RAHYNIVTF) (SEQ_ID_NO:170) were identified, indicating that an A at the second position should be allowed in the HLA-A24 motif. All these inclusions are indicated in Table 20-e. In analyzing these tables it can be concluded that between 2 and 7 high affinity binding peptides were identified for all of the tested HLA-A molecules. Occasionally some peptides were binding to more alleles. Three peptides (E6-7, E6-37 and E6-79), bound to HLA-A2.1, A3.2 and A11.2. One peptide (E6-38) bound to HLA-A3.2, A11.2 and A24 and two peptides (E6-69 and E6-80) bound to HLA-A1, A3.2 and A11.2. But these crossreactive peptides bound only weakly to one or more of the different HLA molecules. In general, however, it can be concluded that, except for HLA-A3.2 and HLA-A11.2 molecules, almost all HLA molecules bind unique peptides.

Please replace the paragraph beginning on page 87, line 34 with the following paragraph:

All of the references cited herein, including patents, patent applications, and publications, are hereby incorporated in their entireties by reference.

Pending pages 50-54 were replaced with the attached substitute pages 50-54.

Pending pages 88-97 were replaced with the attached substitute pages 88-97.

Pending pages 103-117 were replaced with the attached substitute pages 103-117.

50

For HLA-A11 (A*1101):

- 1 XTXXXXXXX
- 2 XTXXXXXXXX
- 3 XVXXXXXXX

5 4 XVXXXXXXXXXXXXX

For HLA-A24.1 (A*2401):

- 1 XYXXXXXXX
- 2 XYXXXXXXXX
- 10 3 XYXXXXXXL
 - 4 XYXXXXXXXXL

Peptides with MHC Class I Binding Motifs

Table 9

deleted

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added

	Peptides with MHC	Class	I Binding	Motifs	Table 9
AA	Position Sequence	(ON OID	Äntigen	HLA	molecule
5	30 IHDIILECVY	100	HPV16.E6	A1	
	69 VCDKCLKFY	(2)	HPV16.E6	A1	•
	77 YSKISEYRHY	(3)	HPV16.E6	A1	
	80 ISEYRHYCY	(4)	HPV16.E6	A1	
	92 GTTLEQQYNK	(5)	HPV16.E6	A11	
10	93 TTLBQQYNK	(6)	HPV16.E6	A11	
	106 LLIRCINCQK		HPV16.B6	A3	
	2 HGDTPTLHEY	(8)	HPV16.E7	A1	
	16 QPETTDLYCY		HPV16.E7	A1	
15	44 QAEPDRAHY	(10) l	HPV16.E7	A1	
	89 IVCPICSQK	(11)	HPV16.E7	A3,	A11
	3 RFEDPTRRPY	(12)	HPV18.E6	A1	
	4 FEDPTRRPY	(13)	HPV18.E6	A1	
20	25 LQDIEITCVY	(14)	HPV18.E6	A1	
	41 LTEVFBFAFK	(15)	HPV18.E6	. A11	•
	72 YSRIRBLRHY	(16)	HPV18.E6	A1	· ·
	84 SVYGDTLEK	(17)	HPV18.E6	A3,	A11
	101 LLIRCLRCQK	(18)	HPV18.E6	A3	
25		1 1			
	59 HTMLCMCCK added	(19)	HPV18.E7	A11	

Human Papilloma Virus 16 and 18 (E6 and E7 Proteins)

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	Peptides with MHC (Class I	Binding	Motifs	Table 10
AA	Position Sequence (SEQ IDAG	Antige	en	HLA mo	lecule
5	2 SLEQRSLHCK (20)	MAGE 1		A 3	
	96 SLFRAVITK (21)	MAGE 1		A 3	
	96 SLFRAVITKK/(22)	MAGE 1		A 3	***
	108 DLVGFLLLK ((23)	MAGE 1		A 3	
	128 MLESVIKNYK (24)	MAGE 1	v ·	A 3	
10	128 MLESVIKNY (25)	MAGE 1		A1	
	152 QLVFGIDVK (24)	MAGE 1		A 3	
	161 EADPTGHSY (27)	MAGE 1		A1	•
	182 LLGDNQIMPH (28)	MAGE 1		A3	
	215 WEELSVMEVY (29)	MAGE 1		A1	
15	223 VYDGREHSAY (30)	MAGE 1		A1	
	238 LLTQDLVQEK (31)	MAGE 1		A 3	
	239 LTQDLVQEK (32)	MAGE 1		A11	
	239 LTQDLVQEKY (33)	MAGE 1		A1	
	240 TQDLVQEKY (34)	MAGE 1		A1	
20					

Melanoma Antigen MAGE 1

53

	Peptides with	MHC	Class I	Binding	Motifs	Table 11	L
	added _						
AA	Position Sequence (Se	EQ ID NO	:))Antige	n	HLA	molecule	
			1				
5	21 IVGGWECEK	(35)	PSA		АЗ,	A11	
	57 LTAAHCIRNK	(36)	PSA		A11		
	88 VSHSFPHPLY	(37)	PSA		A 1		
	95 PLYDMSLLK	(38)	PSA		A 3		
	178 DVCAQVHPQK	(39)	PSA	· · ·	АЗ,	A11	
10	182 QVHPQKVTK	(46)	PSA		A3,	A11	
	236 PSLYTKVVHY	(41)	PSA		A 1		
	239 YTKVVHYRK	(42)	PSA		A11		
	241 KVVHYRKWIK	(43)	PSA		A3,	A11	
•	242 VVHYRKWIK	(44)/	PSA		АЗ,	A11	
15	(

Prostate Specific Antigen (PSA)

54

Peptides with MHC Class I Binding Motifs Table 12

	added			
AA	Position Sequence (SEQID	NO:)\Antige	n HLA molecule	
		/		
5	2 STNPKPQRK \ (4s	HCV	A11	
	14 NTNRRPQDVK (46) HCV	A11	
	43 RLGVRATRK (47) HCV	А3	
	302 VQDCNCSIY (48)	HCV	` A1	
	556 WMNSTGFTK (49)) HCV	А3	
10	605 LTPRCMVDY (50)	HCV	~ A1	: .
	626 FTIFKIRMY (51)	HCV	A1	
	\	<i>/</i> .		

Hepatitis C Virus (Consensus Sequence)



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TABLE 13

VALIDATION OF CYTEL'S HLA MOTIFS

			acity (IC				- /	ad
Sequence	e Motif	Al	A2.1	A3.2	A11	A24	SEQ ID NO:	
aadkaaaa	Y Al	50				. •• i	57	1.
atakaaa	Y A1	15	• •	329	77	•-	58	1
ATDKAAAA	Y A1	2.8	• •	9250	840	ND	<i>5</i> 9	
ALAKAAA	V A2.1		125	- +			60	
LLLARAMA	K A3.2	**		48	8.4	·	61	
ATAAAAA	AK A11		•	59	40	•	62	
AYAKAAN	AF A24		••			115	63 /	

•

TABLE 14

20 validation of CYTEL'S HLA MOTIFS

		8	inding Capaci	ty (IC ₅₀ nM)		
SEQUE	ENCE (SED ID)	MOTIF	A1 .	A2.1	A3.2	All
	(64)	Al	45	-		•
ATAKA!	UAAY (65)	A1	58	′	1100	1030
ATDKAJ	MAAY (64)	A1	4.0	••	10000	4533
	(F4) VAAA		ND	1400		• •
AMAAA	AAAAK (68)	A3.2.	ND	••	85	24.0
ATAAA	AAAAK (69)	All	••	••	216	88.
-		-				

*A dash indicates an IC₅₀ greater than 20,000 nM.

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Version with markings to show changes made

TABLE 15

HLA-A3.2

added

						٦ ١
5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION	SER I	D
	952.25	alaaaaaak	1	-	70	-
	952.26	амалалалк	1.2	position 2	61	1
	952.23	AVAAAAAAK	0.95		71	٦
	981.04	ASAAAAAK	0.89		72	1
10	952.24	AIAAAAAAK	0.57		73	1
	952.27	аааааааак	0.57		74	7
•	981.06	атаааааак	0.49		62	1
	981.08	AFAAAAAAK	0.13	-	75	1
	981.09	AGAAAAAK	0.077		76	1
15	981.13	ACAAAAAAK	0.031		77	1
	981.12	ADAAAAAK	0.014		78]
	981.11	ANAAAAAAK	0.0010		79	1
	981.05	акаааааак	<0.0016		80	
	981.07	AYAAAAAAK	<0.0005	·	81]
20	981.10	APAAAAAAK	<0.0006		8.5	
	952.35	ALAAAAAAR	0.46	position 9	83	
	981.36	ALAAAAAAY	0.15		84	
	981.33	ALAAAAAA	0.0034	·	85	
	981.35	ALAAAAAAQ	<0.0006		86	1
25.	981.37	ALAAAAAAS	<0.0005	r	87	
	981.38	ALAAAAAAT	<0.0005		88	1
	981.34	ALAAAAAAN	<0.0005		89	1
	981.39	ALAAAAAAE	<0.0003		90],
						- /

TABLE 16

HLA-A11

added

					(
5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION	SEC ID
	952.25	ALAAAAAAK	1	-	1 70
	952.26	AMAAAAAAK	2.5	position 2	61
	952.27	AAAAAAAAK	1.1		74
	952.24	AIAAAAAK	0.72		73
10	981.06	АТААААААК	0.55		62
	981.04	ASAAAAAK	0.46		72
	981.09	AGAAAAAAK	0.38		76
	952.23	AVAAAAAK	0.23		71
	981.11	ANAAAAAK	0.23		79
15	981.13	АСААААААК	0.019		77
	981.08	АГААААААК	0.020		75
	981.12	ADAAAAAK	0.012		78
	981.05	АКААААААК	0.0065		80
	981.07	АУААААААК	<0.0065		81
20	981.10	АРААААААК	<0.0051		82
	952.35	ALAAAAAAR	0.015	position 9	83
	981.33	ALAAAAAA	<0.0059		85
	981.34	ALAAAAAAN	<0.0071		89
	981.35	ALAAAAAQ	<0.0051		86
25	981.36	ALAAAAAAY	<0.0071		84
	981.37	ALAAAAAAS	<0.0051	· · · · · · · · · · · · · · · · · · ·	87
	981.38	ALAAAAAAT	<0.0051		8.8
	981.39	ALAAAAAE	<0.0071		90

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Version with markings to show changes made

TABLE 17

HLA-A24

added

•					
5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 983.01	SUBSTITUTION	SEQID NO:
	983.01	ачакаааар	1	-	63
	983.08	AFAKAAAAF	0.24	position 2	91
	983.09	аракалаағ	0.0058		92
	983.10	AAAKAAAAF	0.0023		93
0	983.11	AKAKAAAAF	<0.0012		94
	983.05	AYAKAAAAI	0.20	position 9	95
	983.04	AYAKAAAAL	0.11		96
	983.06	AYAKAAAAV	0.0023		97
	983.02	ачакалала	<0.0012		98
.5	983.03	АУАКААААУ	<0.0012		99
	983.07	AYAKAAAAK	<0.0012		100

		<u>Version</u> v	<u>with markings to show</u>		
			TABLE 18	-	adde
			HLA-Al		add
5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION	SEQ ID
				SOBSTITUTION	NO:
	982.011	ATDKAAAAY	Motif	•	59
	982.07	ATAKAAAAY	1	-	58
	982.09	ASAKAAAAY	0.17	position 2	101
	982.13	AMAKAAAAY	0.095	no D in pos 3	102
.0	982.08	AAAKAAAAY	0.0064		103
	954.09	ALAKAAAAY	0.0045	·	104
	954.11	AIAKAAAAY	0.0045		105
	954.13	AVAKAAAAY	0.0020		106
	982.10	AKAKAAAAY	0.0011		F01
.5	982.11	ANAKAAAAY	<0.0001		108
	982.12	ADAKAAAAY	<0.0001		109
	982.14	AGAKAAAAY	<0.0001	-	110
	982.15	АРАКААААЎ	<0.0001		111
	982.16	АУАКААААУ	<0.0001		99
0	982.17	Анакаааау	<0.0001		112
	982.24	Атакааааа	0.0040	- position 9	113
	982.23	ATAKAAAAF	0.0019	no D in pos 3	114
	982.28	Атакаааан	0.0010		115
	982.32	ATAKAAAAV	0.0005		116
25	982.25	ATAKAAAAN	<0.0001		117
	982.26	ATAKAAAAD	<0.0001		118
	982.27	ATAKAAAAW	<0.0001		119
	982.30	АТАКААААК	<0.0001		120
	982.31	АТАКААААІ	<0.0001		121

<0.0001

30

982.29

АТАКААААР.

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Version with markings to show changes made

		A 61 21011 M	<u>ith markings to snow ch</u>	langes made	
			TABLE 19		. 1
			HLA-A1		adde
	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION	SEG ID
	982.01	ATDKAAAAY	Motif		59
	982.07	ATAKAAAAY	1	-	58
	982.01	AADKAAAAY	0.14	position 3	57
	954.03	AAEKAAAAY	0.038	no T in pos 2	123
	982.02	AAAKAAAAY	0.0055		103
	982.06	AASKAAAAY	0.0024		124
	982.04	AANKAAAAY	0.0011		125
	982.03	AAQKAAAAY	0.0008	-	126
	982.05	AAKKAAAAY	<0.0001		127
٠	982.20	AADKAAAAA	0.0016	position 9	128
	982.21	AADKAAAAW	0.0005	no T in pos 2	129
	982.19	AADKAAAAF	<0.0001		130
	982.22	AADKAAAAK	<0.0001		131

TABLE 20(A)

HPV16 E6 AND E7 PEPTIDES BINDING TO HLA-A1

5	Orgin	First aa Position	Sequence	Den in	Binding Ratio	Motif Prediction
	E6	80	ISEYRHYA	(132)	3.500	+
	B6	69	VADKALKF	(133)	0.240	+
	B7	44	QAEPDRAH	x ((134)	0.029	•
10	E7	37	EIDGPAGQ	A (135)	0.025	•
	E7	19	TTDLYAYE	0 (136)	0.023	•
	E6	144	MSAARSSR	т (137)	0.019	+/-
	E7	73	HVDIRTLE	0 (138)	0.014	•
	E6	139	WTGRAMSA	a (139)	0.010	•
15	E6	61	YRDGNPYA	v (140)	0.008	•,

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value tSE of the standard in the course of the experiments considered in this table was 81±30 nM. Listed in the table are peptides yielding ratio values of ≥0.001. All other peptides yielded ratio values of ≤0.001.

TABLE 20(B)
HPV16 E6 and E7 Peptides Binding to HLA-A3.2

		TIL TIO LO AI	id E7 Peptides Billain	g to HLA-AJ.Z	
5	Origin	Pirst aa Position	Sequence No:	inding Ratio	Motif Prediction
	E 6	107	LIRAINAON (141)	3.7000 Ado	lod .
	E 6	59	IVYRDGNPY (142)	3.0000	→
	E7 '	89	INDENTATION (148)	2.2000	+
10	E 6	33	IILEAVYAK (144)	1.5000	+
	E6	125	HLDKKORFH (145)	0.4400	· •
	E 6	143	AMSAARSSR (146)	0.1800	+
	26	. 7	AMFODPOER (147)	0.1000	. •
	E6	93	TTLEQQYNK (148)	0.0780	+
15	E6	37	AVYAKQQLL (149)	0.0320	-
	E7	51	HYNIVTFAA (150)	0.0210	-
	E6	145	SAARSSRTR (151)	0.0200	•
	E6	75	KFYSKISEY (152)	0.0100	+
	E6	89	SLYGTTLEO (153)	0.0080	-
20	E7	52	YNIVTFAAK (154)	0.0067	-
	E6	80	ISEYRHYAY (132)	0.0064	+
	E6	42	QQLLRREVY (155)	0.0058	•
	E6	68	AVADKALKF (15%)	0.0056	•
	E6	97	(157)	0.0045	-
25	E6	79	KISEYRHYA (158)	0.0044	•
	E6	84	RHYAYSLYG (159)	0.0036	•
	E6	69	VADKALKFY (133)	0.0025	+
	E6	146	AARSSRTRR (160)	0.0020	+
	E7	58	AAKADSTLR (161)	0.0016	+
30	E6	38	VYAKQQLLR (162)	0.0012	•
	E6	67	YAVADKALK (163)	0.0012	+
	E7	. 60	KADSTLRLA (164)	0.0012	_

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value \pm SE of the standard in the course of the experiments considered in this table was 30 ± 3 nM. Listed in the table are peptides yielding ratio value of ±0.001 . All other peptides yielded ratio values of ±0.001 .

Table 20(C)

HPV16 E6 and E7 Peptides Binding to HLA-A11.2

5		First aa	(seo in Bir	nding Ratio	Motif
	Orgin	Position		ScandardI	Prediction
	E6	33	IILEAVYAK (149)	6.7000	11.1 +
	E6	93	TTLEQQYNK (148)	1.8000	lded :
	E7	89	IAYLIYZOK (143)	1.3000	+
10	E6	7	AMFODPOER (14 7)	0.8400	+/-
	E6	59	IVYRDGHPY (142)	0.4700	- (+)5
	E6	80	ISEYRHYAY (132)	0.4300	- (+) S
	E6.	37	AVYAKQQLL (149)	0.0450	•
	E6	145	SAARSSRTR (151)	0.0330	+/-
15	E6	107	LIRAINAQK (141)	0.0120	•
	E7	58	AAKADSTLR (161)	0.0110	+/-
	E6	42	QQLLRREVY (155)	0.0084	+/- (+) S
	E6	143	AMSAARSSR (146)	0.0084	•
	E6	79	KISEYRHYA (15B)	0.0076	- ,
20	E6	67	YAVADKALK (163)	0.0074	•
	E7	52	YNIVTFAAK (154)	0.0060	•
	E6	68	AVADKALKF (15%)	0.0037	•
	E6	69	VADKALKEY (133)	0.0030	- (+) 5
	E6	38	VYAKQQLLR (162)	0.0022	+/-
25	E6	140	TGRAMSAAR (165)	0.0012	+/-
	E7	90	VAPIASOKP (166)	0.0012	-
	E7	51	HYNIVTFAA (150)	0.0010	-

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value \pm SE of the standard in the course of the experiments considered in this table was 10 \pm 3 nM. Listed in the table are peptides yielding ratio value of \pm 0.001. All other peptides yielded ratio values of \pm 0.001. Brackets indicate score according to adjusted motif.

Table 20(D)

HPV16 E6 and E7 Peptides Binding to HLA-A24

				100	ance	
5	Orgin	First aa Position			nding Ratio Standard:	Motif Prediction
	E6	87	AYSLYGTTI	(167)	0.1200	+
	E6	72	KALKFYSKI	(168)	0.1100	- (+) \$
	26	131	RFHNIRGRV	(169)	0.1000	+
10	B7	49	RAHYNIVTE	(170)	0.0670	- (+)5
	26	49	VYDFAFRDI	(171)	0.0610	+
	86	82	EYRHYAYSI	(172)	0.0460	•
	B6 ·	26	LQTTIHDI	(173)	0.0200	•
	B 6	66	PYAVADKAI	(174)	0.0055	•
15	E6	1	MHQKRTAMI	(175)	0.0049	•
	E6	85	HYAYSLYG	(176)	0.0037	•
	E6	44	LLRREVYDI	(177)	0.0023	÷
	E6	. 38	VYAKQQLLI	2 (162)	0.0011	<u>.</u>

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 22±6 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of ≤0.001. Brackets indicate score according to adjusted motif.

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		(67																																	
		i	Tabl																																	
	A24										0																									
	A11	0.0002	0	0.028	0.0061	<0.0002		0.0005	0	0	0.012	0.0022	<0.0002 ×	0.011	<0.0002	0.0018	0.72	0000	0.013	0.0097	031	975	0.069	0.052	\$000¢	0.031	0.023	0.0023	Q.074	0.010	3.6	1970	0,22	0.013	0	0.14
	A3.2	0.037	0.0003	0	0	20000>		0.0003	0.0017	0	0.010	<0.0002	0.0012	0.0024	2000°0>	0.76	0.11	0.48	0.40	038	0.28	0.17	0.0007	0.0007	000	0.0015	0.0004	0.019	<0.0002	0.0005	0.043	0.021	93	0.20	0.18	0.14
	A1.	1.6	7.6	0.18	0.13	0.043		2.7	13	1.1	1.1	0.063	0000	0.018	0.012												٠									
	Motif	1	1	1	-	-		-	1	1	1	-	-	-	-	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
	Pos.	7,5	869	104	1131	401		889	898	707	\mathcal{I}	1239	751	53	1014	189	699	852	Ķ	673	167	999	899	74	80%	828	218	714	33.7	209	<u>3</u> 9	222	733	141	048	822
	Molecule																																			
	Strain					>																														
	Virus	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2		c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	∘ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2
	¥	6	6	6	6	6		10	10	2	2	2	2	2	2	6	6	0	6	6	6	6	6	6	6	6	6	6	6	•	10	10	92	01	10	2
	Sequence	HLDMLRHLY	LLDIDETEY	CTOLFEDNY	LTCSPQPEY	ETLEETTGY		FTHQSDVWSY	RLLDIDETEY	TLEETICKLY	YVMAGVGSPY	GTPTAENPEY	LIORNPOLCY	VVQCNLELTY	MGDLVDAEEY	KIRKYTIMIRR	WINCILIKE	LVKSPNHVK	VLRENTSPK	ILIKRRQQK	ILWKDIFHK	KITDFCLAR	CWACILIK	QVCTCTDMIK	LLDHVRENR	CVNCSQFLR	TVCAGGCAR	ILKETELRK	VTAEDGTQR	DLSYMPIWK	TILWKDIFHK	GTQRCEXCSK	KVLRENTSPK	QUESTIERE	RLVHRDLAAR	LLNWCMQIAK
	Peptide	1.0300	1.0346	1.0305	1.0355	1.0317		1.0749	1.0747	1.0715	-	1.0764	1.0705	1.0693	├	1.1028	1.1027	170971	1.0835	1.0329	1.0311	1.1083	1.0869		_	-	1.1023	1.0831	1.1024	1.0326	\vdash			_		1.0741
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	ğ	84	¥.	8	9	182		 68	\$	3	38	<u>E</u>	22	E	6	Ē	5,	ध	ŧ	135	20	#	192	-	8	ā	28	E	お	28	8	Ŕ	3	ğ	22	ā
	(Qreas)	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 A3.000 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.057 0.000	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 1,0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.000 0.000 1,0346 LLDIDETEY 9 c-ERB2 869 1 7.6 0.000 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1,0300 HLDMLRHLY 9 c-ERBZ 42 1 9.1 0.000 0.000 1,0346 LLDIDETEY 9 c-ERBZ 869 1 7.6 0.000 0 1,0305 GTQLFEDNY 9 c-ERBZ 104 1 0.18 0 0.003	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0306 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.0002 0.0002 1.0306 LLDIDETEY 9 c-ERB2 869 1 7.6 0.0003 0 1.0305 CTQLFEDNY 9 c-ERB2 104 1 0.18 0 0.008 1.0355 LTCSPQPEY 9 c-ERB2 1131 1 0.13 0 0.0061	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0304 HLDMLRHLY 9 c-ERB2 869 1 76 0.0002 0 1.0304 LLDIDETEY 9 c-ERB2 869 1 76 0.0003 0 1.0305 CTQLFEDNY 9 c-ERB2 1131 1 0.13 0 0.0061 1.0315 ETLEETICY 9 c-ERB2 - 401 1 0.043 <0.002	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0304 HLDMLRHLY 9 c-ERB2 869 1 76 0.0002 0 1.0304 LLDIDETEY 9 c-ERB2 869 1 76 0.0003 0 1.0305 CTQLFEDNY 9 c-ERB2 1131 1 0.13 0 0.0061 1.0317 ETLEETIGY 9 c-ERB2 0 0.003 c0.003 c0.003	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.002 1.0346 LLDIDETEY 9 c-ERB2 8.69 1 7.6 0.003 0 1.0356 CTQLFEDNY 9 c-ERB2 1.031 1 0.13 0 0.0061 1.0317 ETLEFITGY 9 c-ERB2 4.01 1 0.043 c.0002 1.0317 FTLEFITGY 9 c-ERB2 4.01 1 0.043 c.0002 1.0346 FTHQSDVWSY 10 c-ERB2 4.01 1 2.7 0.0003 0.0005	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 869 1 7.6 0.0002 0.0002 1.0305 CTQLFEDNY 9 c-ERB2 1.031 11 0.13 0 0.0061 1.0317 ETLEFITGY 9 c-ERB2 401 1 0.043 c.0002 1.0317 FTHQSDVWSY 10 c-ERB2 899 1 2.7 0.0002 1.0749 FTHQSDVWSY 10 c-ERB2 889 1 1.3 0.0017 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 869 1 7.6 0.0002 0.0002 1.0346 LLDIDETEY 9 c-ERB2 1.04 1 0.18 0 0.0002 1.0356 LTCSPQPEY 9 c-ERB2 0.0007 1131 1 0.13 0 0.0001 1.0317 ETLEETICY 9 c-ERB2 0.0007 0 0.0001 1.0349 FTHQSDVWSY 10 c-ERB2 0.0007 0 0.0001 1.0347 RLLDIDETEY 10 c-ERB2 0.0007 0 0.0001 1.0347 RLLDIDETEY 10 c-ERB2 0.0007 0 0 0.0001 1.0348 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.0001 1.0349 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0 0.001 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0 0 0 1.0340 TLEETICYLY 10 c-ERB2 0.0017 0 0 0 0 0 0 0 1.0340 TLEETICYLY 10 0.0017 0 0 0 0 0 0 0 0 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.007 0.0002 1.0346 LLDIDETEY 9 c-ERB2 869 1 7.6 0.0002 0 1.0355 LTCSPQPEY 9 c-ERB2 1131 1 0.13 0 0.0081 1.0374 FTHQSDVWSY 10 c-ERB2 . 401 1 0.03 4.0002 A.0002 1.0747 RLLDIDETEY 9 c-ERB2 . 4.01 1 0.03 4.0002 A.0002 1.0747 TLEETGYLY 10 c-ERB2 . 4.01 1 0.003 0 0 1.0757 YVMAGVGSPY 10 c-ERB2 . 772 1 1.1 0.01 0 0 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.007 0.0002 1.0346 LLDIDETEY 9 c-ERB2 869 1 7.6 0.0003 0 1.0355 LTCSPQPEY 9 c-ERB2 131 1 0.13 0 0.0061 1.0357 ETLEFITGY 9 c-ERB2 401 1 0.03 4.00 0 0.0061 1.0374 FTHQSDVWSY 10 c-ERB2 401 1 0.043 4.0002 0 0 1.0747 RLLDIDETEY 10 c-ERB2 602 1 1 0 0 0 0 1.0743 TLEETGYLY 10 c-ERB2 602 1 1 0 0 0 0 0 0 0 0 0 0 0<	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A32 A11 A24 1.0300 HLDMLRHLY 9 c.ERB2 42 1 9.1 0.007 0.0002 0.0002 1.0346 LLDIDETEY 9 c.ERB2 869 1 7.6 0.0003 0 0 1.0355 LTCSPQPEY 9 c.ERB2 , 401 1 0.13 0 0.0061 0 0 1.0377 ETLEGTGY 9 c.ERB2 , 401 1 0.13 0 0.0061 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.0002 0 0 1.0346 LLDIDETEY 9 c-ERB2 104 1 7.6 0.0003 0 0 1.035 LTCSPQPEY 9 c-ERB2 . 401 1 0.13 0 0.0061 0 1.035 LTCSPQPEY 9 c-ERB2 . 401 1 0.13 0 0.0061 0 1.037 FTHQSDVWSY 10 c-ERB2 . 401 1 0.03 <0.0002	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 A	Peptide Sequence AA Virus Strain Molecule Fos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 c-ERB2 42 1 9.1 0.007 0.0002 1.0346 LLDIDETEY 9 c-ERB2 104 1 7.6 0.0003 0 0 1.035 LTCSPQPEY 9 c-ERB2 131 1 0.13 0 0.0061 0	Peptide Sequence AA Virus Strain Molecule Fos. Motif A1 A3.2 A11 A24 1.0300 HLDMLRHLY 9 -cERB2 5 1 9.1 0.000 0 0 1.0346 LLDIDETEY 9 -cERB2 869 1 7.6 0.000 0 0 1.0355 LTCSPQPEY 9 -cERB2 1131 1 0.13 0 0 0 1.0375 LTCSPQPEY 9 -cERB2 401 1 0.13 0 0 0 1.0376 ETLEGTGY 9 -cERB2 401 1 0.13 0 0 0 1.0377 ETLEGTGY 9 -cERB2 401 1 0.03 0 0 0 1.0749 FTHGSDVWSY 10 -cERB2 401 1 0.03 0 0 0 0 1.0749 THEGTGYLY 10 -cERB2	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 1.0500 HLDMLRHLY 9 c-ERB2 1.0500 1.0540 HLDMLRHLY 9 c-ERB2 1.0540 1.0540 1.0570 1.	Peptide Sequence AA Virus Strain Molecule Pos. Moif A1 A32 A11 A24 1.0300 HLDMLRHLY 9 -ERRZ 1 9.1 0.000 0.000 1.0346 LLDIDETEY 9 -ERRZ 869 1 7.6 0.000 0 1.0355 LTEDIDETEY 9 -ERRZ 401 1 0.18 0 0.000 1.0355 LTEGITGY 9 -ERRZ 401 1 0.18 0 0.000 1.0375 LTGENTORY 9 -ERRZ 401 1 0.03 4.000 0 1.0376 LTGENTORY 9 -ERRZ 401 1 0.043 4.000 0 0 1.0376 LTGENTORY 10 -ERRZ 401 1 0.043 4.000 0 0 1.0376 LTGENDVASY 10 -ERRZ 402 1 1 0 0 0	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A32 A11 A24 A10000 A100000 A10000 A10000 A10000 A10000 A10000 A10000 A1000000 A1000000000 A10000000000	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A3.2 A11 A24 A1300 HLDMIRHLY 9 CERR2 1034 1 1 1 1 1 1 1 1 1	Peptide Sequence AA Virus Strain Molecule Pos. Molf A1 A32 A11 A24 1.0300 HLDMLRHLY 9 c-ERBZ 6 1 5.1 9.0 0.0002 0 1.0346 LLDIDETEY 9 c-ERBZ 104 1 1.8 0 0.0003 0 1.0355 LTGSPQFEY 9 c-ERBZ 401 1 0.13 0 0.0005 1.0375 LTGSPQFEY 9 c-ERBZ 401 1 0.13 0 0.0005 1.0375 LTGSPQFEY 9 c-ERBZ 401 1 0.03 4.0002 0 0 1.0376 LTGSPQFEY 9 c-ERBZ 401 1 0.03 0	Peptide Sequence AA Virus Strain Molecule Pos. Molif A1 A3.2 A11 A24 A11 A24 A12 A24 A12 A24 A	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A32 A11 A24 A2	Peptide Sequence AA Virus Strain Molecule Pos. Molf AJ AJ AJ AJ 1.0346 HLDMLRHLY 9 -ERBZ 6.6 1 7.6 0.000 0 1.0346 LLDIDETEY 9 -ERBZ 104 1 0.18 0 0.000 1.0346 LLDIDETEY 9 -ERBZ 104 1 0.18 0 0.000 1.0355 LTCSPQPEY 9 -ERBZ 401 1 0.18 0 0.006 1.0377 FTHQSDVWSY 10 -ERBZ 89 1 2.7 0.000 0 1.0779 FTHQSDVWSY 10 -ERBZ 88 1 1.3 0 0 1.0779 FTHQSDVWSY 10 -ERBZ 88 1 2.7 0.000 0 1.0779 FTHQSDVWSY 10 -ERBZ 88 1 1.1 0 0 1.0771	Peptide Sequence AA Virus Strain Molecule Pcs. Motif A1 A3.2 A11 A24 1.000 HLDMLRHLY 9 cERRZ 6.0 1 7.6 0.000 0 1.004 HLDMLRHLY 9 cERRZ 1.0 1 7.6 0.000 0 1.004 LLDIDEFIEY 9 cERRZ 1.0 1 7.6 0.000 0 1.005 LTCSPQPEY 9 cERRZ 4.0 1 0.18 0 0 0 1.007 LTCSPQPEY 9 cERRZ 4.0 1 0.18 0 0 0 1.007 LTCSPQPEY 9 cERRZ 4.0 1 1 0.18 0 0 0 1.007 LTCSPQPEY 9 cERRZ 4.0 1 1 0.0 0 0 0 0 0 0 0 0 0 0 0 0	Peptide Sequence AA Virus Strain Molecule Pos. Molif A1 A3.2 A11 A24 1.000 HLDMLRHLY 9 cERBZ 6.9 1 7.6 0.000 0 1.004 HLDMLRHLY 9 cERBZ 89 1 7.6 0.000 0 1.005 LLDIDETEN 9 cERBZ 104 1 0.18 0 0.006 1.005 LTGPOPEN 9 cERBZ 1131 1 0.18 0 0 0.0061 1.007 FTHCEDTOYLY 10 cERBZ 899 1 2.7 0.0002 0.0061 1.007 FTHCEDTOYLY 10 cERBZ 899 1 2.7 0.0002 0.0061 1.007 FTHCSDVWSY 10 cERBZ 899 1 2.7 0.0002 0.0061 1.007 FTHCSDVWSY 10 cERBZ 899 1 2.7 0.0002 0.0061<	Peptide Sequence AA Virus Strain Molecule Fos. Molif AJ AJJ AJJ<	Peptide Sequence AA Virus Strain Molecule Pos. Motif A1 A32 A11 A24 1.000 HLDMLRHLY 9 c-EREZ 869 1 7.6 0.000 0	Peptide Sequence AA Virus Strain Molecule Fos. Molif AJ AJ AJ 1.0304 HLDMICHLY 9 cEREZ 42 1 9.1 0.00 0.00 1.0304 LLDIDETEY 9 cEREZ 69 1 7.6 0.000 0 1.0305 LLOSOPEY 9 cEREZ 401 1 0.13 0 0.006 1.0375 LUCROPEY 9 cEREZ 401 1 0.13 0 0.006 1.0376 CTOLLEDAY 9 cEREZ 401 1 0.13 0 0.006 1.0376 CTOLLEDAY 9 cEREZ 401 1 0.13 0 0.006 1.0376 CTOLLEDAY 9 cEREZ 402 1 1 0.13 0 0.006 1.0376 CTOLLEDAY 9 cEREZ 402 1 1 0.00 0 0 0 <	Peptide Sequence AA Virus Strain Molecule Fos. Molif AJ AJJ AAJ 1.0346 LLDIDETEY 9 -EBBZ 89 1 7.6 0.000 0 1.0346 LLDIDETEY 9 -EBBZ 89 1 7.6 0.000 0 1.0346 LLDIDETEY 9 -EBBZ 103 1 0.13 0 0.000 1.035 LLCSPOPEY 9 -EBBZ 103 1 0.13 0 0.006 1.037 TALENTOY 9 -EBBZ 401 1 0.13 0 0.006 1.037 TALENTOYLY 9 -EBBZ 401 1 0.03 4.000 0 0 1.037 TALENTOYLY 10 -EBBZ 401 1 0.13 0 0.006 0 0 0 0 0 0 0 0 0 0 0 0 0	Peptide Sequence AA Virus Strain Molecule Pos. Mole AI AI AIA AA AIII AA3 AII AA3 AII AA34 AIII AA34 AIIII AA34 AIIII AA34 AIIII AA34 AIIII AA34	Peptide Sequence AA Virus Sirain Molecule Fos. Molf AJ AJ AJ AJ 1.000 HLDMIRHLY 9 ceRRZ CR 1 51 0.000 0.000 1.004 LLDDEFIEY 9 ceRRZ CR 1 51 0.000 0.000 1.005 GTQLEDWY 9 ceRRZ 0.00 1 7.6 0.000 0 1.005 GTGLEDWY 9 ceRRZ 0.01 1 0.03 0 0.000 1.007 GTGLEDWY 9 ceRRZ 0.01 1 0.03 0 0 1.007 GTGLEDWY 9 ceRRZ 0.01 1 0.03 0 0 0 1.007 GTGRA D 0.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 <td>Peptide Sequence AA Virus Strain Molecule Fos. Molif A1 A32 A11 A24 1.0346 LLIDDETEY 9 c-ERRZ 89 1 7.6 0.000 0 1.0346 LLIDDETEY 9 c-ERRZ 89 1 7.6 0.000 0 1.0345 LLICSROPEY 9 c-ERRZ 40 1 0.13 0 0.006 1.0375 LLICSROPEY 9 c-ERRZ 40 1 0.03 0 0 1.0376 FTH-GENTOY 9 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOY 9 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOYSPY 10 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOYSPY 10 c-ERRZ 40 1 0.04 0 0 1.0377</td> <td> Peptide Sequence AA Virus Strain Molecule Pos. Molif A1 A2 A1 A2 A1 A2 A3 A3 A3 A3 A3 A3 A3</td>	Peptide Sequence AA Virus Strain Molecule Fos. Molif A1 A32 A11 A24 1.0346 LLIDDETEY 9 c-ERRZ 89 1 7.6 0.000 0 1.0346 LLIDDETEY 9 c-ERRZ 89 1 7.6 0.000 0 1.0345 LLICSROPEY 9 c-ERRZ 40 1 0.13 0 0.006 1.0375 LLICSROPEY 9 c-ERRZ 40 1 0.03 0 0 1.0376 FTH-GENTOY 9 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOY 9 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOYSPY 10 c-ERRZ 40 1 0.04 0 0 1.0376 FTH-GENTOYSPY 10 c-ERRZ 40 1 0.04 0 0 1.0377	Peptide Sequence AA Virus Strain Molecule Pos. Molif A1 A2 A1 A2 A1 A2 A3 A3 A3 A3 A3 A3 A3

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		(//	(3(a)	70.0	med	\ \ \ \ \	Į								,		-		
				Table 23(a)	1000	Ē	10000													
		A24												ļ -						
	į	AII	0.11	0.0072	0.075	0.072	0.0005	0.033	0.033	0.0042	9100	0.0014	0.013	0	0.0099					
		A3.2	0.057	0.082	0.017	0.0005	0.040	0.0072	0.018	000	0.0030	0.015	0.0068	0.011	0.0009					
	;	AI																		
	7.7	ros. Mont	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11					
			713	851	423	478	148	226	88	296	699	229	217	88	747					
		Molecuie																		
		Strain	•																	
	V:	Virus	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2	c-ERB2				`	
		44	10	10	10	10	10	10	10	10	10	10	10	10	10		a .			
	, The second sec	Sednence	RILKETELRK	VLVKSPNHVK	SVFQNLQVIR	HTVPWDQLFR	ILKGGVLIQR	LVSEFSRMAR	GVVFGILIKR	CVARCPSGVK	WPCILIKRR	GILIKRROOK	RTVCAGGCAR	GLACHQLCAR	KIPVAIKVLR		_		•	
	Donaide	repuae	1.0731	1.0745	1.1131	1.1133	1.1127	1.1143	1.1136	1.0726	1.1137	1.0728	1.1129	1.1134	1.1139					
(ā 3	·	213	214	215	216	4 %	218	77	220	122	222	223	727	225)			

		411.0	idos c						
A24									
A11					0.61	0.12	0.034	0.21	950.0
A3.2					0.30	0.31	0.048	0.010	9200:0
A1.	0.016	0.010	0.015	0.014					
Motif	-	-	-	-	3,11	3,11	3,11	3,11	3,11
Pos.	607	553	4 08	501	Š	514	578	267	523
Molecule Pos. Motif									
Strain									
Virus	EBNA1	EBNAI	EBNAI	EBNA1	EBNA1	EBNA1	EBNA1	EBNA1	EBNA1
. V	6	6	2	2	٥	6	٥	2	92
Sequence	VCEADYFEY	PLRESIVCY	PVGEADYFEY	CTWVACVFVY	GVFVYGGSK	KTSLYNLRR	AIKDLVMTK	QTHIFAEVLK	GTALAIPOCR
Peptide	1.0201	1.0295	1.0681	1.0683	1.0293	1.1016	1.0297	1.0687	1.1124

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22.62 22.82 22.82 23.22 23.23

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Table 23(c)

																	. ;		
A24																	2.9	0.031	0.15
A11			0.0037	0.062	0.10	0.0000	0.041	0:030	0.024	0.84	0.0079	0.037	0.0046	0.016	0	0.010			
A3.2			1.5	Ø.0	0.031	0.059	0.0016	16000	87000	0.12	0.50	0.36	0.019	0.0018	0.012	1000			
. Y	3.6	0.020																	
Motif	1	-	3	3	3	3	3	3	3	3	3	3	3	3	3	3	24	24	24
Pos.	14	228	365	. 122	991	32	99	\$	200	165	31	264	175	376	382	જ	39	218	33
Molecule	ΝP	NP	ΔN	Νb	ďN	ďZ	ďN	ď	NP	NP	NP	NP	NP	NP	ΝP	ď	ďŽ	ď	dΝ
Strain	٧	<	4	<	∢	ď	4	∢	<	¥	Ą	٧	٧	Y	4	4	V	4	٧
Virus	FLU	FLU	FLU.	F.U	FLU	E.U.	FLU	E.U	FLU	FLU	FLU	FLU	FLU	FLU	FLU	EU.	FLU	FLU	FLU
AA	6	6	6	٥	٥	٥	٥	٥	۵	2	2	01	01	01	2	2	6	٥	20
Sequence	CTELKISDY	STLELRSRY	ILRCSVAHK	RMCNILKGK	LMQCSTLPR	MIDGIGREY	MVLSAFDER	YIQMCTELK	GINDRNFWR	SLMOGSTLPR	KMIDCICRFY	LILRCSVAHK	RSGAAGAAVK	SSTLELRSRY	RSRYWAIRTR	RMVLSAFDER	PYIQMCTEL	AYERMONIL	RFYIQMCTEL
Peptide	5.0005	5.000.6	5.0044	5.0051	5.0046	5.0048	5.0049	5.0054	5.0042	5.0104	5:0095	9600'5	5.010.2	5.010.5	5.0103	5.0101	5.0061	5.0060	5.0112

SEG ID NO:

		<u>.</u>	1abe 2										····•					- ,			·							·		·									
	A24						L. L. Samenanian and L. Samena															0.0017		٥	00001		0	0					٥		۰				
	A11	0	0.0006	•	•	٥	0.0075		0.014					\$000 \$				1	0	٥	0.0037	000	6012	g	635	EOGI	868	8000	0	0	٥	٥	Q.017	0	0200	<0.0002			
	A3.2	0.0007	0.0087	0.0008	-0,000B	0	0.0003		0.30					<0.0002					0	972	400009	0.014	0.0056	659	83	0.0087	1 00	0.15	200	٥	<0.0005	0	0.019	0	0.033	<0.0002			
	A1	25 ·	17.2	13	0.85	0.77	0.50	0.045	0.068	0.067	0.057	0.054	0.025	0.019	0.017	0.013	1100	0.0097	11.1	6.3	4.2	==	=	99.0	0.57	0.37	र ह	0.30	0.21	0.20	0.20	0.16	0.15	0.12	11.0	0.081	0.066	0:030	0.018
	Motif	1	1	-	-	1	1	-	-	1	1	1	1	-	. 1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-		1	1	1	1	1	-	-	-
	Pos.	420	1001	1,382	1,521	1382	1280	1280	629	1,550	\$	316	188	869	1092	466	1,364	1,036	419	120	1,000	1250	1087	1,098	1098	1,067	1069	1,069	120	887	1,035	869	292	1279	738	416	288	23	972
	Molecule	CORE	PQ.			10	POL	æ	POL					P0l.	POL				CORE	ENV		POL	POL		ğ		<u>3</u>		ES	EN EN		POL		POL.		CORE		M	
	Strain	adr	adr	YIF	adr.	adr	wpe	wbo	adr	wpe	аум	wpe	wbs	• adr	wpe	MÁB	adr/adw	adr.	adr.	adr.	YTL	adr.	wys	adw	wbe	wie	-tg	adr	wbs	adw	.pe	adr	WYB	wpe	adr/adw	мрв	wye	adr	sdr
	Virus	HBV	HBV	HBV	HBA	HBV	HBV	46	HBV	HEV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV
	\$	•	•	6	6	6	6	0	6	٥	۵	6	6	6	6	6	6	6	10	10	10	10	10	10	10	01	20	2	10	10	10	10	10	2	10	22	10	10	10
	Sedneuce	LLDTASALY	SLDVSAAFY	PTTGRTSLY	MSTTDLEAY	PTTGRTSLY	LTKOYLNLY	LTRATLALY	KVGNFTGLY	MSPTDLEAY	PSQPSRGNY	PSSWAFAKY	CSAVRKEAY	PLDKGIKPY	SLMLLYKTY	ASRDLVVSY	PSRGRLGLY	SSTSRNIINY	DILLDTASALY	LLDPRVRCLY	ISLDVSAAFY	FLCQQYLHLY	QTFGRKLHLY	KTYGRKLHLY	KTYCRKLHLY	OTFGRICHLY	KTECRICHILY	KTFCRKLHLY	LODPRVRALY	TTPAQCTSMY	LSSTSRNINY	PLDKGIKPYY	HSASPCCSPY	FLTKOYLNLY	RSASPCCSPY	WLWGMDIDPY	TTPAQCTSMY	HTLWKAGILY	TSCPPICPCY
	Peptide	1 0155		1	1	1		202				ŀ			ı	20115	20124	20121	1.0519	1.0513	20239	1.0911	91207	20244	1620:1	20042	1.0556	2.0241	1.0766	1.0806	2.0240	1.0541	20238	1.0795	20237	1.0774	20233	1.0542	20231
- ر	SBRID	7 254	552	256	25.7	188	300	200	282	760	3	262	253	787	245	377	433	248	592	270	拉	242	233	芸	77.4	243	242	StZ	25%	45	3	3	82	281	787	83	442	B	282

Peptide 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0910 1.0010 1		X 2 2 2 0 0 0 0 0 2 2 2 2 3 3 3 3 3 3 3 3	Virus HBV HBV HBV HBV HBV HBW HBW HBW HBW HBW HBW HBW	Strain adw adr adr ayw ayw ayw ayw ayw ayw ayw ALL	Molecule POL	Pos. 11,161 1,161 1059 2584 887 295 295 295	Motif	A1 0.016 0.015 0.0004	A3.2	A11	A24 0.0005
Peptide		\$ 22200000002222	Virus HIBV HIBV HIBV HIBV HIBV HIBV HIBV HIBV	adv adv ayw ayw ayw ayw ayw ayw ayw ALL	الدوري والمنازك التواكل الثان الأواكات التواكا التواكا التواكا	Pos. 11,161 1,161 1,166 1,166 1,166 1,166 1,166 1,166 1,166 1,167	Motif		A3.2	A11	A24 0.0005
2,0246 2,0069 2,		000000000000000000000000000000000000000	HBV HBV HBV HBV HBV HBV HBV HBV HBV HBV	adr adr ayw ayw ayw adr/adw ayw ayw adr/adw	FOL POL POL POL POL POL POL	1,161 1059 1084 713 867 887 887 887 887 887 887 887 887 887		0.016			0.0005
1.0910 1.0910 2.0089 2.0089 2.0089 2.0024 2.0024 2.0089		200000000000000000000000000000000000000	HBV HBV HBV HBV HBV HBV HBV HBV HBV HBV	adr ayw ayw ayw adr/adw ayw ayw ayw	POL	1059 11084 11197 11197 11197		0.0004			0.0005
2,0089 2,0089 2,0086 2,0086 2,0086 2,0089 2,		0 0 0 0 0 0 0 0	HBV HBV HBV HBV HBV HBV HBV HBV HBV HBV	ayw ayw ayw ayw adr/adw ayw ayw	FOL POL POL	29 295 295 295 295 295 295 295 295 295 295	2 8 8 8 8 8 8 8	0.000			0.0005
2.0069 2.0116 2.0116 2.0067 2.0067 2.0069 2.	- - - - - - - - - - - - - -	00000222	180 НВИ НВИ НВИ НВИ НВИ НВИ НВИ НВИ НВИ НВИ	ayw ayw ayw adr/adw ayw ayw ayw	POL POL POL POL POL POL POL	1084 713 867 887 887 1197 11197			0.00	٥	
2,0066 2,0067 2,0077 2,0077 2,0077 2,0077 2,0074 2,0069 2,	├─┼─┠─┠─╂─╂─╂─╂	6 6 6 9 9 9 9	HBV HBV HBV HBV HBV HBV HBV HBV HBV HBV	ayw ayw adr/adw ayw ayw ayw	701. 701. 701. 701.	713 887 887 1197 1197 295 295			1.8	0.64	
2,0062 2,0066 2,0077 2,0077 2,0077 2,0077 2,0077 2,0074 2,0069 2,	╎╴╏╸╏╺╏╺╏╺╏╸╏╸╏╸╏	0000000	HBV HBV HBV HBV HBV HBV	ayw ayw adr/adw ayw ayw ayw	POL POL POL POL	867 886 1197 1197 295 295			660	1.5	
5.0056 2.0077 2.0019 2.0024 2.0024 2.0036 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0039 2.0044 2.0050	┠╌┞╼╂═╂╼╂╾╂╶╂╶╂	00000	HBV HBV HBV HBV HBV	ayw ayw adr/adw ayw ayw	POL POL POL	331 1197 1197 295 295			0.14	0.025	
2,0077 2,0234 2,0234 2,0234 2,0334 2,0334 2,0044 2,	┠╸┨╺╏╸╏╸╏╸╏	v 5 5 5 5	HBV HBV HBV HBV HBV	ayw ayw adr/adw ayw ayw	701. .POL .POL	295 295	m m m m		<0.0003	2900	
2023 2024 2023 2024 2024 2024 2006 2006 2006 2006 2006	╂═╂╌╂╌╂╌╂	2222	HBV HBV HBV HBV	ayw adr/adw ayw ayw ALL	POL	295	E E E		0.041	\$4000	
2,0024 2,0024 2,0024 2,0024 2,0024 2,0034 2,0036 2,0039 2,	╂╼╂═╂═╂	222	HBV HBV HBV	ayw ayw ayw ALL	POL	282 582	E E		96.0	7.4	
2,0235 5,0107 2,0245 5,0108 2,0084 2,0086 2,0086 2,0087 2,0089	┠╸╏╶╏╶╏	22	HBV HBV	ayw syw ALL	POL	562	6		0.43	61	
\$0107 20245 20245 \$50108 20094 20049 20049 20049 20049 20049 20049 20049 20049 20049 20049 20049 20040 2	 	2	HBV	syw ALL	POL	1	,		11	1.79	
2,0245 5,0108 2,0084 2,0084 2,0085 2,0085 2,0085 2,0085 2,0089 2,	MEGRIK		HBV	ayw ALL	POL	8	m		0.15	13	
2,0045 2,0004 2,	WLGAK	2		ALL		200	3		6870	1200	
\$5,006 2,0094 2,0065 2,0065 2,0066 2,0066 2,0069 2,		2	HBV			1,123	.3		0.16	0.0076	
2008 2006 2006 2006 2006 2008 2008 2008	SWKR	 92	HBV.	-	POL	뚌	6		9000'0	6.013	
20069 20069 20069 20069 20069 20089 20089 20089 20089 20080	PTYKAFLCK	6	HBV	wye	30.	1263	n		0.030	0.085	
2006 2006 2006 2006 2008 2008 2008 2008	PTDLEAYFK	_	HBV	.wpa	×	1552	=		200010	0.016	
2,0069 2,0046 2,0049 2,0049 2,0049 2,0049 2,0049 2,0060 2,	PWLL	9	HBV	ALL		1,330	24				3.6
2,0046 2,0049 2,0049 2,0049 2,0049 2,0046 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0047 2,0048 2,0047 2,0047 2,0047 2,0047 2,0048 2,0047 2,	LYAAVTINFL	6	HBV	wpe		1,169	24				3.2
2,0045 2,0049 2,0049 2,0044 2,0046 2,0050 2,0050 2,0060 2,	LTKYL	6	HBV	adr.		68 9	24				2.1
2.0049 2.0049 2.0049 2.0044 2.0059 2.0050 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060 2.0060	LYSSTVPSF	6	HBV	adw/ayw		599	24				1.9
2,0049 2,0089 2,0081 2,0081 2,0087 2,0087 2,0082 2,0082 2,0083 2,	FYPKVTKYL	6	HBV	wyw		718	24				1.7
2,0089 2,0044 2,0089 2,0081 2,0080 2,	TKYL.	6	HBV	wpe		718	24				1.6
2,004 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008 2,008	SPFL	6	HBV	wke		398	24				050
2,0089 2,0051 2,0060 2,0060 5,0062 2,0064 2,0063 2,0063 2,0063	VPVL	6	HBV	adr		989	24				0.37
2,0051 2,0060 2,0060 5,0062 2,0064 2,0063 2,0063 2,0063	SPFL	6	HBV	adr		368	24				0.34
2,0060 2,0047 2,0060 5,0062 2,0064 2,0043 2,0043	SWPKF	٥	АВН	ayw		8	24				0.18
2,0047 2,0060 5,0062 2,0064 2,0043 2,0181	RHM	6	HBV	adw/ayw		743	24				0.15
2.0062 2.0062 2.0054 2.0043 2.0181	RHM	6	HBV	adr		74	24				0.057
5.0062 2.0054 2.0043 2.0181	MPLY	6	ABH	ALL		1,224	24	٠			0.049
2.0054	PNAPI		HBV	Z	NUCXNUCFUS	131	24				97070
2.0043	CRKL	5	АВИ	ayw.		1,085	24				4100
2.0181	FREL	6	HBV	ayw		209	24				0.011
00000	-	2	A9F	ALL		1,077	24				1.1
2.0182	LYAAVINFLL	2	HBV	adw		1,169	24				0.32
321 20188 LYRPLISLPF	Н	2	HBV	adr		1,371	24				0.25
2.0174	\vdash	10	HBV	wye		709	22				91.0
323 2.0173 SYQHFRKILI	-	01	HBV	adr/adw		238	24				9900

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A24	0.040	0.022	0.01	0.0099																																	
A11					7.4	0.30	0,40	13	0.010	0.83	0.92	0.92	0.7 1	070070	¥60	\$000	0.41	0.40	033	0.20	0.28	62	0.017	8	0.034	0.048	0.018	0.003	0.098	0.0002	<0.0005 40.0005	0.082	0.076	0.0045	0.0032	0.019	0.0002
A3.2					0.31	5.0	2.5	400	17	000	0.0006	0.39	0.17	250	150	0.44	0000	0.016	0000	0011	0.10	0.0039	g	0011	0.18	0.16	0.11	0.10	6	898	000	0.042	2002	0,002	0,068	0.065	0.064
Ā						•																															
Motif	24	24	24	24	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
Pos.	735	521	234	572	1090	1066	1095	722	719	899	1523	1061	1274	1257	æ	1488	1197	8 2	740	w	1505	683	828	8	1259	202	1230	§	Ē	989 899	730	1548	129	1065	757	1550	786
Molecule				POL	POL	POL	POL	POL	POL	POL	"X"	POL	PQL	POL	ENA	х.	POL	PQL	POL	ENA	χ.	POL	POL	POL	Z Z	CORE	POL	POL	POL	POL	POL	.x.	POL	POL	POL	.x.	POL
Strain	wya	ALL	. ALL		wpe	adr	wpe	wpe	adr	adw	adr	adr	wbe	adr	wpe	adr.	adr	wpe	wbs	adr	adr	adr	adw	sdr.	wpe	аум	adr	adr	adr	adr	adr	adr	adr	adr	.pg	adr	wpe
Virus	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	HBV	ABH .	HBV	HBV	HBV	HBV
\$	2	. 01	10	2	6	6	٥	9	6	٥	6	6	۵	6	6	6	6	6	6	6	6	6	6	6	. 6	6	6	6	6	6	6	6	6	٥	6	6	6
Sequence	YYPEHLVNHY	AYRPPNAPIL	GYRWMCLRRF	NFLISLGIHL	YVSLMILYK	LLYKTFGRK	LYKTYGRK	VTKYLPLDK	RHYLHTLWK	STVPSFNPK	TTDLEAYFK	YYSLLLYK	PTYKAFLTK	HLYPVAROR	STNRQLGRK	ALRFTSARR	PVNRPIDWK	TVNENKRLK	VVNHYPQTR	STISTGPCK	OVLPKILHK	LTKYLPLDK	CLHQSAVRK	WDFSQFSR	PLYACIQAK	YVNTNIMGLK	PLYACIQSK	RLADEGLNR	AVNHYFKTR	RLKLIMPAR	ILYKRETTR	KVFVLGGCR	NVSIPWTHK	LLLYKTFCR	RLVFQTSTR	FVLGGCRHK	RLVLOTSTR
Peptide	2.0176	20172	17102	5.0115	1.0377	1.0189	1.0379	1.0370	1.0176	1.0867	1.0215	1.0848	1.0383	1.0967	1.0358	1.0991	1.0197	1.0369	1.1041	1.0152	1.0213	1.0172	1.0374	1.0980	1.0382	20074	1.0199	1.0972	1.0976	1.0975	1.0977	1.0993	1.0165	1.0982	1.0978	1.0219	1.1042
2:02 2:02	X	325	326	327	328	32	330	33.	332	333	334	335	33%	455	338	133	340	7	345	348	344	345	346	347	348	34	350	35	352	2	5	B	325	33	388	5	5

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40000	
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22 23	7 E 8
» Pol	POL
adw adv	adw Ape
HBV HBV	AB 1
2 2 2	2 2 2
VLSCWWLQFR NVTKYLPLDK RVCCOLDPAR	SLGIHLNPOK
1.0781	1.0793
374	388
	1.0935 VLSCWWLQFR 10 1.0781 NVTKYLPLDK 10

added

_	_										1	1(0)																					
17/2007	(0)573501	/continued /		added								-					Table 2261																		
						A24								0.0002		1.4	0.026	0.010																	
	0.014	0.0024	0.010	0.0095		A11	0.010	0.010	0.0003					0.0034	0.0024				0.87	0.033	0.16	0.19	0.010	5000	0.038	0.033	0.0079	0.011	1:1	0.0051	0.012	0.025	0.13	0.032	٩
	0000	0.013	<0.0003	0.0025		A3.2	0	0	0.0005					0.013	0.11				9000	6.73	0.74	0.54	0.25	91.0	0.016	00019	0.015	0.0095	0.87	0.57	20	0.0	0.17	60003	0.015
1						A1	3.0	09.0	0.54	0.078	0.053	650:0	0.012	0.41	0.30																				
	3,11	+	╁	3,11		Motif	-	-	-	1	1	1	1	1	1	24	24	24	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
	\$ 5	1185	314	702		Pos	1123	269	302	605	2588	2416	979	2888	1617	719	633	719	5269	290	43	1391	1390	51	1183	2563	2241	1042	1858	1227	632	1390	1361	3002	723
	20 Z	JOJ.	S S	POL		Molecule	LORF	NS1/ENV2			LORF	LORF		LORF	LORF		-		LORF	ENVI	CORE	LORF	LORF	CORE	LORF	LORF	LORF	LORF	LORF	LORF	NS1/ENV2	LORF	LORF	LORF	NS1/ENV2
	adr.	adr	adw	wpe		Strain																						•							
	ABA Page	IBY	HBV	HBV		Virus	ΗÇ	ΗŽ	HCV	HCV	HCV	HCV	HCV	HCV	HCV	HCV	нсу	HCV	HCV	HCV	HCV	HCV	нсл	HÇ	HCV	ΗÇ	HCV	HCV	HCV	HCV	HCV	HÇ	HCV	HCV	HCV
	2 2	2 2	2	10		4	0	0	٥	6	٥	6	6	9	2	6	2	10	6	6	6	6	6	6	6	6	6	6	10	10	2	10	01	10	10
1000	YVGPLTVNEK RI ADECI NEE	IVLKLKOCFR	PIPSSWAFAK	LTVNENRRLK		Sequence	CTCCSSDLY	NIVDVQYLY	VQDQNGSIY	LTPRCMVDY	RVCEKMALY	DVVCCSMSY	FTIFKIRMY	GLSAFSLHSY	TLHCPIPLLY	EWLLFL	MYVGGVEHRL	EWILLFLL	SVPAEILRK	QLFTPSPRR	RLCVRATRK	LIPCHSKKK	HLIPCHSKK	KTSERSOPR	AVCTRGVAK	EVRCVQPEK	TRVESENK	CUTSLTGR	GVACALVAFK	HLHAPTGSGK	RMYVGGVEHR	HLIPCHSKKK	TLCFGAYMSK	GVGMLLPNR	LLFLLLADAR
	1.0535	801	1.0773	1.0778		Pentide	1,0118	1.0112	20034	20035	1.0145	1.0140	20036	1.0509	1.0489	20087	20169	20170	1.0139	1.0955	1.0090	1.0123	1.0122	1.0952	1.0120	1.0143	1.0137	1.0957	1.0496	1.0480	1.1062	1.0485	1.0484	1.1067	1.1063
1	£ 5	Ş	50	463	(A		- So	ş	\$	89	503	ş	Ŧ	두	Ę	Ţ	4.5	915	ţ	等	<u>.</u>	9	ž	424	43	#2#	122	424	424	824	423	丹	£3	432

NO: Peptide Sequence AA

3-8 120207 FVCPLTVNEK 10

A11 0.015

A3.2

A1

Pos. Motif 698. 3,11

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23(f)	
Table	

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A24											0.76	0.33	8	070	0.052	0.03	0.013	0.017	0.014	0.014																
A11			00056	0.0004	0.0030					120	•										0000	1.8	98.0	0.37	0.77	0.065	0.16	0000	8698	980	0.057	<0.0005	0.066	0000	900	0.0048
A3.2			400000	0	00007					5	3										27	0.17	11	0068	0.013	020	0.0091	0.12	<u>g</u>	0.064	0.077	0.007	0.012	0,003	0.0021	000
A1	0.090	900	0.018	0.28	0.25	0.088	0.053	0.039	0.013	0.013																										
Motif	-	-	_	-	-	-	-	-	-	- '	,	\$ 70	\$ 2	2 22	77	24	24	24	24	24	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	211
Pos.	867	8	æ	ෂ	874	2	1187	1329	1345	742	754	27/3	1 022	183	1,036	1,036	875	266	266	% %	138	<u>5</u>	8	1075	177	88	1215	443	1458	925	1227	₹	1111	752	2420	200
Molecule	CAG		POL	δĹ	POL		POL	POL	POL												POL	70L	POL	POL	VIF	POL	POL	CAG	POL	10.I	POL	CAC	POL	POL	ENA	0.0
Strain																																				
Virus	HIV	нгу	нгу	HIV	HIV	HIV	HΙΛ	HIV	AIH .	AIF	HIV		≩ į	711	Æ	H	HIV	HIV	HILA	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	AIIA	HIV	HIV	HΙΣ	HIV	ΑIV	HIV	ΛIH	
\$	6	0	6	20	2	92	2	10	10	2	2	6	۰,	۰ ،	-	۵	۵	2	2	2	6	6	6	6	٥	6	6	6	٥	6	۵	6	6	٥	6	
Sequence	FRDYVDRFY	IYQYMDDLY	TVLDVGDAY	VTVLDVGDAY	VIYOYMDDLY	VTVLDVGDAY	EVNIVIDSQY	LVAVHVASGY	PAETGQETAY	ISKICPENPY	OMAVEIHNEK	RYLKDOOLL	RYLKDOOLL	TYONOEPE	DOEPFIONE	IYOEPFICH	IYOYMDDLY	TYKRWIILGIL	NYRWIILGL	LYPLASILESI	KLAGRWPVK	AVFIHNFKR	AIPOSSMITK	IVIWGKTPK	KLTEDRWNK	GIPHPAGLK	QIIEQLIKK	KIWPSYKCR	LATDIQTK	MCYELHPOK	YLAWVPAHK	KIWPSHKGR	FVNTPPLVK	NTPVFAJKK	TVQCTHGIK	
Peptide	1.0014	2.0129	1.0028	1.0412	1.0415	2022	1.0431	1.0441	1.0462	20251	20025	7002		20065		4	7008	2027	20190	20249	+	1.0944	1.0082	1.0046	-	1.0027	1.0059	1.0939	1.0072	1.0086	1.0062	1.0938	1.0047	1.0024	1.0080	
SES ID	33	事	S	A A	曹	ğ	85	5	Ş	Ī	12	\$	£3	*	1	F S	7	\$	3	毕	448	Ş	5	F	5	4	4	育	35	阜	55	\$	3	19	462	

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			V	1 lable	T. 4.		<i>]</i> :	Dag	 ,															
A24																								
A11	0.040	0.040	0.032	0.030	0.0039	0.016	7.8	5.6	0.85	0.78	0.090	9/2010	0.024	0.21	0.17	0.082	0.055	0.038	0.021	0.0013	0.019	0.015	0.012	0.011
. A3 .2	0.0007	<0.0009	0.038	110.0	67070	<0.0008	3.8	0.16	99.0	95'0	15'0	0.39	0.32	0.032	ดดา	0.056	0.0099	0.015	<0.0005	0700	0.0024	<0.0002	0.0002	<0.0002
A1																								
Motif	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
Pos	82	1199	1254	692	1513	ર્જી	2185	335	2	1253	768	\$	440	1474	88	1117	642	628	1504	04	2741	606	729	327
Molecule	CAG	POL	POL	POL	POL	POL	PN	POL.	POL	POL	<u>2</u>	POL	GAG	POL	70L	POL	POL	POL	POL	CAC	ENV	POL	POL	CAC
Strain																								
Virus	HIV	ΑĪ	ΑIA	HIV	HIV	HZ	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV	HIV
*	۰	6	6	6	6	6	2	2	2	2	2	2	2	2	2	2	စ္က	2	2	2	2	2	2	2
Sequence	RDYVDRFYK	GIIQAQPDK	VLFLDGIDK	LVDFRELNK	KVVPRRKAK	MTKILEPFR	TVYYGVPVWK	TVQPIVLPEK	AVFIHINFKRK	KVLFLDGIDK	KLVDFKELNK	KLKPGMDGPK	FLCKIWPSYK	KIQNFRVYYR	GIPHPAGLKK	LVKLWYQLEK	MICGICCFIK	MTKILEPFRK	VVIQDINSDIK	FLCKIWPSHK	IVOCONNLLR	FTTPDKKHQK	LVEICTEMEK	LVQNANPDCK
eptide	1.0015	1.0058	1.0064	1.0026	1.0008	1.0942	1.0463	1.0418	1.0447	1.0437	1.0408	1.0403	1.0395	1.1056	1.0410	1.0426	1.0398	1.0413	1.0453	1.0394	1.1069	1.0417	1.0405	1.0392

added

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Table 23(g)

Peptide Sequence AA Virus Strain Molecule Pos. Motif AI A32 A41 1.0223 SERTRINCY 9 HPY 16 ES 80 1 73 0.003 6.0000 2.0163 SERTRINCY 9 HPY 16 ES 7 1 0.02 6.0000 0.00 2.0163 SENTRINCY 10 HPY 16 ES 7 1 0.02 6.0000 0.00 2.0163 SEXESTRAHY 10 HPY 16 ES 7 1 0.00 0.00 0.00 2.0163 HGDITALHEY 10 HPY 16 ES 7 1 0.00 0.00 0.00 1.059 HGDITALHEY 10 HPY 16 ES 7 1 0.00 0.00 0.00 1.059 HGDITALHEY 10 HPY 16 ES 7 1 0.00 0.00 0.0	Seare				•								
10022 SEPRINYCY 9 HPP 16 EB 9 1 78 0.00 0.00 10023 CARDINANIA 9 HPPV 16 E 5 1 0.22 0.00 0.00 10429 CARDINANIA 9 HPPV 16 E 5 1 0.25 0.00 0.00 2.0159 VEXICENTRAY 10 HPPV 16 E 5 1 0.02 0.00 0.00 1.090 HPPV 16 E 5 1 0.01 0.00 0.00 0.00 1.090 HPPV 16 E 5 1 0.00	ğ	Peptide	Sequence	¥	Virus	Strain	Molecule	Pos.		A1	A3.2	A11	A24
1,10290 OMEPIDAMY 9 HPV 16 E 4 1 0.021 0.0002<	88	1.0225	ISEYRHYCY	٩	HPV	16	93	88		7.8	1100.0	92070	
10460 LODIENTOY 10 HPP 18 ES 25 1 0.25 0.0056 0.0071 20163 YSKSENRHY 10 HPV 16 ES 77 1 0.11 6.0000 0 20163 YSKSENRHY 10 HPV 16 ES 7 1 0.017 6.0000 0 1.0893 HCDITILLY 10 HPV 16 ES 30 1 0.025 6.0000 0 1.0894 AVCDKCLKY 10 HPV 16 ES 30 1 0.003 0	15	1	QAEPDRAHY	ď	HPV	91	B	4		0.021	<0.0092	<0.0002	
20163 YKKEEVRHY 10 HPV 16 E6 7 1 0.17 4,000 0 1.0803 YKKEEVRHY 10 HPV 16 E7 1 0.013 4,000 1.0801 YCRATULINCY 10 HPV 16 E 1 0.033 4,000 1.0901 YCRATULINCY 10 HPV 16 E 1 0.033 4,000 2.0164 YKRRELRHY 10 HPV 16 E 1 0.033 4,000 2.0164 YKRRELRHY 10 HPV 18 E 7 1 0.013 4,000 2.0164 YKRRELRHY 10 HPV 18 E 7 1 0.013 4,000 2,000 2.0164 YKRRELRHY 10 HPV 18 E 3 1 0.019 4,000 2,000 2,000 2,000 2 1 0.019 4,000 2,000 2 1 <th>3</th> <th></th> <th>LQDIEITCVY</th> <th>2</th> <th>HPV</th> <th>18</th> <th>93</th> <th>25</th> <th>1</th> <th>0.25</th> <th>9500.0</th> <th>0.012</th> <th></th>	3		LQDIEITCVY	2	HPV	18	93	25	1	0.25	9500.0	0.012	
2.016.2 YSKSEPRHY 10 HPV 16 EB 7 1 0.002 0.002 1.0893 HGCHTLHEY 10 HPV 16 EB 2 1 0.003 0.002 1.0893 HGCHTLLYY 10 HPV 16 EB 3 1 0.003 0.003 2.0163 YSKIRELRYY 10 HPV 16 EB 3 1 0.003 0.003 2.0164 YSKIRELRYY 10 HPV 18 EB 10 0.003 0.003 2.0164 YSKIRELRYY 10 HPV 18 EB 10 0.003 0.003 2.0164 YSKIRELRYY 10 HPV 18 EB 10 0.003 0.003 2.0164 YSKIRELRYY 10 HPV 18 EB 3 2 1 0.003 0.003 2.0027 LIRCANC 9 HPV 18 EB 8 1 0.003	Ţ	1	YSKISEYRHY	9	HPV	91	93	7	1	0.17	<0.0009	0	
10599 HCDITPLIHEY 10 HPV 16 EP 2 1 0.0597 0.0007 0.00	ţ	ı	YSKISEYRHY	2	HPV	16	ង	11	1	0.11	<0.0009	0	
10601 CPETIDLYCY 10 HPV 16 E 6 1 0.032 0.032 10894 YCDKCLKCY 10 HPV 16 E 6 1 0.0025 0.0022 0.009 2016 YSGNELRHY 10 HPV 18 E 6 1 0.018 0.009 0.009 2016 YSGNELRHY 10 HPV 18 E 72 1 0.018 0.009 2016 YSGNELRHY 10 HPV 18 E 72 1 0.018 0.009 2016 YSGNELRHY 10 HPV 18 E 72 1 0.018 0.009 2016 YSGNELRHY 10 HPV 18 E 8 73 1 0.019 0.009 2002 YACHURC 9 HPV 18 E 8 31 0.00 0.009 1.00 2003 YACHURC 9 HPV	482	1 1	HCDTPTLHEY	20	НРУ	16	Œ	2	-	0.087	<0.0002	<0.0002	
1.0913 IHDILLECYY 10 HPV 16 E6 30 1 0.0032 0.0072 1.0594 YAVDKCLKFY 10 HPV 16 E6 72 1 0.0093 40002 2.0164 YSKRELRHY 10 HPV 18 E6 72 1 0.009 4000 2.0164 YSKRELRHY 10 HPV 18 E6 10 0.001 0.009 4000 2.0164 YSKRELRHY 10 HPV 18 E6 10 3 0.001 0.009 0.009 2.0164 YSKRELRHY 10 HPV 18 E6 10 3 0.000 0.009 0.009 2.0163 LIRCARCOCK 9 HPV 18 E6 80 3.1 0.000 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009 0.009	+13	1	QPETTDLYCY	2	НРV	91	<i>G</i>	16	-	0.033			
10594 AVCDKCLKPY 10 HPV 16 E6 7 1 0.0055 0.0052 0.0020 20164 YSRIBELHYY 10 HPV 18 E6 72 1 0.013 4.0002 20164 YSRIBELHYY 10 HPV 18 E6 10 0.019 0.009 0.009 20164 YSRIBELHYY 10 HPV 18 E6 10 0.019 0.009 0.009 20082 HTMCANCX 9 HPV 18 E6 9 11 0.019 0.009 20082 VYCKYLL 9 HPV 16 E6 9 24 C 7 20083 VYCKYLL 9 HPV 16 E6 9 24 C 7 20084 VYDARROC 9 HPV 16 E6 9 24 C 7 1 20084 VYDARROC 9 HPV 18 E6	季	1	IHDIILECVY	2	НРУ	91	99	ક્ષ	-	0.032			
20160 YSRIELRHY 10 HPY 18 E6 72 1 0.018 4,0007 4,0007 20164 YSRIELRHY 10 HPY 18 E6 10 1 0.079 0.079 20164 YSRIELRHY 10 HPY 18 E6 10 0.079 0.079 20022 YYCKTVLEL 9 HPY 16 E6 97 24 0.079 0.079 20022 YYCKTVLEL 9 HPY 16 E6 97 24 0.079 0.079 20029 YYCKTVLEL 9 HPY 16 E6 97 24 0.079 0.079 20029 YYCKTVLEL 9 HPY 16 E6 97 24 0 17 <t< th=""><th>\$</th><th></th><th>AVCDKCLKFY</th><th>2</th><th>HPV</th><th>91</th><th>93</th><th>89</th><th>1</th><th>0.0095</th><th>0.0052</th><th>610.0</th><th></th></t<>	\$		AVCDKCLKFY	2	HPV	91	93	89	1	0.0095	0.0052	610.0	
20164 YSRIRELRIY 10 HPV 18 E6 70 1 0.00 0.07 2.0164 HIMCLACKOK 10 HPV 18 E6 33 24 0.00 0.079 2.0022 HIMCLACKOK 9 HPV 18 E6 33 24 0.00 0.079 2.0022 VYCKTVLL 9 HPV 16 E6 87 24 0.00 0.079 2.0024 VYCRTVLECL 9 HPV 16 E6 87 24 0.00 0.079 2.0024 VYCRTVLECL 9 HPV 16 E6 87 3.1 0.00 0.079 2.0029 VYCRTVLECL 9 HPV 18 E6 87 3.1 0.00 0.07 1.0229 VYCRTVLECL 9 HPV 18 E6 89 3.1 0.00 0.05 1.0229 VYCRTVLECK 9 HPV 18 E6 89 <th>415</th> <th>1</th> <th>YSRURELRHY</th> <th>2</th> <th>HIPV</th> <th>18</th> <th>93</th> <th>z</th> <th>1</th> <th>0.018</th> <th><0.0002</th> <th><0.0002</th> <th></th>	415	1	YSRURELRHY	2	HIPV	18	93	z	1	0.018	<0.0002	<0.0002	
2.016.1 LIRCLRCQK 10 HPV 18 E6 101 3 0.081 0.078 2.0032 HTMLCLMCCK 9 HPV 18 E6 33 2.4 0.020 0.079 2.0032 HTMLCLMCCK 9 HPV 16 E6 87 2.4 0.079 0.079 2.0032 CYSLYGTIL 9 HPV 16 E6 89 2.4 0 1.7 1.7 2.0031 LYDEAREDL 9 HPV 16 E6 89 2.4 0 1.7 </th <th>£ 55</th> <th>1</th> <th>YSRIRELRHY</th> <th>92</th> <th>HPV</th> <th>18</th> <th>93</th> <th>2</th> <th>1</th> <th>0.012</th> <th></th> <th></th> <th></th>	£ 55	1	YSRIRELRHY	92	HPV	18	93	2	1	0.012			
20022 HTMLCMCKCK 9 HPW 18 E 59 11 0.020 0.079 20023 VYCKTVILE 9 HPW 18 E 33 24 C 1 20024 VYCKTVILE 9 HPW 16 E 9 24 C 1 20031 LYMLIRGL 9 HPW 18 E 89 24 C 1 20030 VYCDTLEKL 9 HPW 18 E 89 3.1 G 24 1,0229 SYYCDTLEK 9 HPW 18 E 89 3.1 G 3.1 1,0239 SYYCDTLEK 9 HPW 18 E 89 3.11 G 3.2 1,0234 LYMLLKCH 9 HPW 18 E 89 3.11 G 3.2 1,0241 STHAACHK 9 HPW 18 E 89 3.11 0.009 <td< th=""><th>444</th><th></th><th>LLIRCLRCOK</th><th>2</th><th>HPV</th><th>18</th><th>E6</th><th>101</th><th>3</th><th>-</th><th>0.081</th><th>0.078</th><th></th></td<>	444		LLIRCLRCOK	2	HPV	18	E6	101	3	-	0.081	0.078	
20020 VYCKTVLEL 9 HPV 18 E6 37 24 C 20027 CYSLYGTIL 9 HPV 16 E6 87 24 C 20030 VYGDTLBACL 9 HPV 18 E6 87 24 C 20030 VYGDTLBACL 9 HPV 18 E6 87 3,11 0.39 2.3 1,0239 SYYGDTLBAC 9 HPV 18 E6 84 3,11 0.39 2.3 1,0239 SYYGDTLBAC 9 HPV 18 E6 84 3,11 0.39 1.3 1,0239 SYYGDTLBAC 9 HPV 18 E6 84 3,11 0.39 1.3 1,0239 TURZAC 9 HPV 18 E6 89 3,11 0.00 0.35 1,0241 STRIAACHK 9 HPV 18 E6 89 3,11 0.00 0.03 <tr< th=""><th>7</th><th>1</th><th>HTMLCMCCK</th><th>٥</th><th>HPV</th><th>18</th><th>Б</th><th>83</th><th>11</th><th></th><th>0.020</th><th>0.079</th><th></th></tr<>	7	1	HTMLCMCCK	٥	HPV	18	Б	83	11		0.020	0.079	
20027 CYSLYGTIL 9 HPV 16 66 9 24 7 20034 VYOPAARDL 9 HPV 16 66 49 24 7 20031 VYOPAARDL 9 HPV 18 66 98 24 7 20030 VYGOTLECL 9 HPV 18 66 84 3.11 0.39 2.3 1.0243 SYYGOTLECL 9 HPV 18 66 84 3.11 0.39 2.3 1.0244 SYYGOTLECL 9 HPV 18 66 84 3.11 0.30 0.35 1.0244 SYYGOTLECL 9 HPV 18 66 84 3.11 0.30 0.35 1.0244 SYYGOTLECL 9 HPV 18 66 84 3.11 0.30 0.35 1.0245 FILLACLACH 9 HPV 18 66 83 3.11 0.30 0.31	499		WCKTVLEL	6	HPV	18	93	33	24				0.33
20024 VYDPAREDL 9 HPY 16 66 96 24 7 20031 LYNLIRGL 9 HPY 18 E6 98 24 7 20030 LYNLIRGL 9 HPY 18 E6 94 3.11 0.39 2.3 1,0239 SYYCDTLEK 9 HPY 18 E6 84 3.11 0.39 2.3 1,024 SYYCDTLEK 9 HPY 18 E6 84 3.11 0.09 0.95 1,024 SYYCDTLEK 9 HPY 18 E6 84 3.11 0.00 0.95 1,024 SYYCDTLEK 9 HPY 18 E6 89 3.11 0.00 0.95 1,024 SYYCDTLEK 9 HPY 18 E6 89 3.11 0.00 0.95 1.11 1,024 STILLECYNCK 9 HPY 18 E6 33 3.11 0.00	88		CYSLYGTIL	٥	HPV	16	99	82	24				0.057
2.0031 LYNLLIRGL 9 HPV 18 E6 98 24 7 2.0030 VYGJTLIRGL 9 HPV 18 E6 84 3,11 0.39 1.23 1.0235 SYCGJTLER 9 HPV 18 E6 84 3,11 0.09 1.23 1.0244 SYCGJTLER 9 HPV 18 E6 89 3,11 0.07 0.55 1.23 1.0241 SYCGJTLER 9 HPV 18 E6 89 3,11 0.07 0.55 1.23 1.0241 SIPHAACHK 9 HPV 18 E6 89 3,11 0.07 0.25 0.25 1.0245 SIPHAACHK 9 HPV 18 E6 89 3,11 0.07 0.25 0.00 1.0245 SIPHAACHK 9 HPV 18 E6 89 3,11 0.07 0.25 0.00 1.0256 JRCPCSOK 9	ğ		VYDFAFRDL	6	HPV	91	93	6\$	24				0.032
20080 VYCOTLEKL 9 HPV 18 E6 84 3,11 0.39 2.3 1,0229 SVYCOTLEK 9 HPV 18 E6 84 3,11 0.39 2.3 1,0243 SVYCOTLEK 9 HPV 18 E6 84 3,11 0.07 0.55 1,1 1,0244 SVYCOTLEK 9 HPV 18 E6 84 3,11 0.07 0.55 1,1 1,0244 SVYCOTLEK 9 HPV 18 E6 89 3,11 0.07 0.55 1,1 0.07 0.55 1,1 0.07 0.07 0.55 1,1 0.07 0.07 0.55 1,1 0.07 0.07 0.55 0.07 0.05 0.07 0.07 0.05 0.07 0.05 0.07 0.05 0.07 0.05 0.07 0.05 0.07 0.07 0.05 0.07 0.07 0.07 0.05 0.07 0.05 0.07	505		LYNLLIRCL	6	HPV	18	93	86	24				0.019
10243 SYYCDTLEK 9 HPV 18 EG 84 3,11 0.39 10243 SYYCDTLEK 9 HPV 18 EG 84 3,11 0.50 10244 SYYCDTLEK 9 HPV 18 EG 84 3,11 0.07 10224 TLEQOYNK 9 HPV 16 EG 89 3,11 0.00 10241 SIPHAACHK 9 HPV 18 EG 89 3,11 0.00 1024 SIPHAACHK 9 HPV 18 EG 89 3,11 0.00 1025 SIPHAACHK 9 HPV 18 EG 89 3,11 0.00 1026 SIPHAACHK 9 HPV 18 EG 89 3,11 0.00 1029 HPV 18 EG 89 3,11 0.00 10 1029 CTDEYSKIK 9 HPV 18 EG 81	503		VYCDILEKL	6	HPV	91	93	88	24				0.010
10243 SYYGDTLEK 9 HPV 18 E6 84 3,11 0.50 10244 SYYGDTLEK 9 HPV 16 E6 93 3,11 0.00 10224 TTLEQQYNK 9 HPV 16 E6 59 3,11 0.00 10234 SIPHAACHK 9 HPV 18 E6 59 3,11 0.00 10234 SIPHAACHK 9 HPV 16 E6 59 3,11 0.00 10234 SIPHAACHK 9 HPV 16 E6 59 3,11 0.00 10234 FIRCLRCQK 9 HPV 16 E6 3,11 0.00 10234 FIRCLRCQK 9 HPV 16 E6 3,11 0.00 10659 CIDFYSRIR 9 HPV 16 E6 3,11 0.00 10656 CIDFYSRIR 9 HPV 16 E6 3,11 0.00	7		SYNCOTLEK	6	HPV	18	93	ಪ	3,11		660	ន	
1,0224 SVYCDTLEK 9 HPV 16 E6 94 3,11 0.00 1,0224 TILEQQYNK 9 HPV 16 E6 99 3,11 0.0094 1,0231 SIPHAACHK 9 HPV 18 E6 99 3,11 0.0094 1,0232 SIPHAACHK 9 HPV 16 E7 89 3,11 0.0094 1,0233 VCPPCSQK 9 HPV 18 E6 177 3,11 0.0054 1,0294 LIRCLRCQK 9 HPV 18 E6 33 3,11 0.0076 1,0294 LIRCLRCQK 9 HPV 18 E6 83 3,11 0.0076 1,0654 LIRCLRCQK 10 HPV 18 E6 3,11 0.0076 1,0656 LIRCLRCQK 10 HPV 18 E6 3,11 0.0076 1,0656 LIRCLRCQK 10 HPV 18 E6	B		SVYCDILEK	6	HPV	81	93	æ	3,11		0.55		
1,0234 TTLEQQNK 9 HPV 16 E6 99 3,11 0,009 1,0234 SIPHAACHK 9 HPV 18 E6 59 3,11 0,009 1,0234 SIPHAACHK 9 HPV 16 E6 99 3,11 0,009 1,0234 IVCPICSQK 9 HPV 18 E6 177 3,11 0,009 1,0354 ILIECVYCK 9 HPV 18 E6 33 3,11 0,009 1,0359 ILIECYYCK 9 HPV 18 E6 83 3,11 0,009 1,0359 ILIECYYCK 9 HPV 18 E6 33 3,11 0,009 1,0369 CTIPYSRIR 9 HPV 18 E6 33 0,009 1,036 CTIPYSRIR 9 HPV 18 E6 31 0,009 1,059 LIRCLECQK 10 HPV 18 E6 31	Z,		SVYCDILEK	6	HPV	18	93	ळ	3,11		0.70 0.70	85	
10224 SIPHAACHK 9 HPV 18 E6 59 3,11 0.0094 10225 SIPHAACHK 9 HPV 16 E9 3,11 0.005 10223 IVCPICSQK 9 HPV 16 E9 3,11 0.005 1.0997 KIZHIANEKR 9 HPV 18 E6 117 3,11 0.0016 1.0974 LIRCLRCQK 9 HPV 18 E6 33 3,11 0.0016 1.0853 ILIECYYCK 9 HPV 16 E6 83 3,11 0.0016 1.0898 CIDPYSRIR 9 HPV 18 E6 83 3,11 0.0016 1.0898 CIDPYSRIR 9 HPV 16 E6 83 3,11 0.0016 1.0898 CIDPYSRIR 9 HPV 16 E6 93 3,11 0.0016 1.0698 CIDPYSRIR 9 HPV 16 E6	205	1	TTLEQQYNK	6	HPV	16	酱	g	3,11		0.010	290	
10223 SIPHAACHK 9 HPV 16 56 3,11 0,007 10234 NCPICSQK 9 HPV 16 E 89 3,11 0,005 1,0997 KIRHIANEKR 9 HPV 18 E 117 3,11 0,001 1,0234 LIRCLRCQK 9 HPV 18 E 68 3,11 0,001 1,0853 ILECYYCK 9 HPV 18 E 68 3,11 0,001 1,0898 CIDFYSRIR 9 HPV 18 E 68 3,11 0,001 1,0898 CIDFYSRIR 9 HPV 18 E 68 3,11 0,001 1,0898 CIDFYSRIR 9 HPV 16 E 68 3,11 0,001 1,0696 CITLEQQYNK 10 HPV 18 E 10 3,11 0,001 1,0696 LIRCLRCQK 10 HPV 18 E <th>ğ</th> <th></th> <th>SIPHAACHK</th> <th>6</th> <th>НРУ</th> <th>18</th> <th>超</th> <th>æ</th> <th>3,11</th> <th></th> <th>16000</th> <th>025</th> <th></th>	ğ		SIPHAACHK	6	НРУ	18	超	æ	3,11		16000	025	
10923 IVCPICSQK 9 HPV 16 E6 311 0.085 1.0997 KCRHILNEKR 9 HPV 18 E6 117 3,11 0.019 1.0224 LIRCLRCQK 9 HPV 18 E6 33 3,11 0.0016 1.0853 IILECYYCK 9 HPV 16 E6 68 3,11 0.0016 1.0898 CIDPTSRIR 9 HPV 18 E6 68 3,11 0.0016 1.0896 CIDPTSRIR 9 HPV 16 E6 82 3,11 0.0016 1.0896 CITLEQQYNK 10 HPV 16 E6 92 3,11 0.0016 1.0696 LIRCLRCQK 10 HPV 16 E6 10 3,11 0.0016 1.0696 LIRCLRCQK 10 HPV 16 E6 10 3,11 0.006 1.0697 LIRCLRCQK 10 HPV 16 <th>Š</th> <th>1</th> <th>SIPHAACHK</th> <th>6</th> <th>HPV</th> <th>18</th> <th>33</th> <th>SS</th> <th>3,11</th> <th></th> <th>0.017</th> <th>0.12</th> <th></th>	Š	1	SIPHAACHK	6	HPV	18	33	SS	3,11		0.017	0.12	
1,0997 KCRHLNEKR 9 HPV 18 E6 117 3,11 0,005 1,0224 LIRCLRCQK 9 HPV 18 E6 33 3,11 0,0016 1,0853 IILECYYCK 9 HPV 16 E6 68 3,11 0,0016 1,0898 CIDPTSRIR 9 HPV 16 E6 68 3,11 0,0016 1,0896 CIDPTSRIR 9 HPV 16 E6 83 3,11 0,0016 1,0696 CITLEQQYNK 10 HPV 16 E6 92 3,11 0,0016 1,0696 LIRCLRCQK 10 HPV 16 E6 101 3,11 0,0016 1,0696 LIRCLRCQK 10 HPV 16 E6 101 3,11 0,0016 1,0696 LIRCLRCQK 10 HPV 18 E6 10 3,11 0,0007 1,0695 LIRCLRCQK 10 H	405		IVCPICSOK	6	НРУ	16	Э	26	3,11		0.035	6200	
1.00234 LIRCLRCQK 9 HFV 16 E6 3.11 0.0016 1.0853 IILECVYCK 9 HFV 16 E6 33 3,11 0.0016 1.0996 CIDFTSRIR 9 HFV 18 E6 68 3,11 0.0016 1.0996 CIDFTSRIR 9 HFV 16 E6 83 3,11 0.0016 1.0696 CITLECQYNK 10 HFV 16 E6 92 3,11 0.010 1.0696 CITLECQYNK 10 HFV 16 E6 92 3,11 0.010 1.0696 LIRCLRCQK 10 HFV 16 E6 10 3,11 0.006 1.0629 LIRCLRCQK 10 HFV 18 E6 10 3,11 0.006 1.0614 LIEVEFEAR 10 HFV 16 E6 41 3,11 0.006 1.0626 LIEVEFEAR 10 HFV 16 </th <th>208</th> <th>, ,</th> <th>KLKHLNEKR</th> <th>٥</th> <th>НРУ</th> <th>18</th> <th>.E6</th> <th>Ξ</th> <th>3,11</th> <th></th> <th>0.025</th> <th><0.0005</th> <th></th>	208	, ,	KLKHLNEKR	٥	НРУ	18	.E6	Ξ	3,11		0.025	<0.0005	
1,0853 IILECYYCK 9 HPV 16 E6 33 3,11 0,0016 1,0999 CIDFISRIR 9 HPY 18 E6 68 3,11 0,017 1,0998 CIDFISRIR 9 HPY 16 E6 82 3,11 0,010 1,0596 CITLEQQYNK 10 HPY 16 E6 101 3,11 0,010 1,0598 LIRCLRÇQK 10 HPY 16 E6 101 3,11 0,016 1,0599 LIRCLRÇQK 10 HPY 16 E6 101 3,11 0,016 1,0599 LIRCLRÇQK 10 HPY 18 E6 101 3,11 0,16 1,0629 LIRCLRÇQK 10 HPY 18 E6 41 3,11 0,16 1,0649 LIRCLRÇQK 10 HPY 16 E6 41 3,11 0,007 1,0649 LIRCLRÇQK 10 HPY <th>505</th> <th></th> <th>LIRCLINCOK</th> <th>6</th> <th>HPV</th> <th>18</th> <th>E6</th> <th>102</th> <th>3,11</th> <th></th> <th>910.0</th> <th>0.0012</th> <th></th>	505		LIRCLINCOK	6	HPV	18	E 6	102	3,11		910.0	0.0012	
1.0999 CIDFTSRIR 9 HPV 18 E6 68 3,11 0.007 1.0998 CIDFTSRIR 9 HPV 18 E6 83 3,11 0.010 1.0596 GTTLEQQYNK 10 HPV 16 E6 92 3,11 0.010 1.0608 LIRCINCQK 10 HPV 16 E6 101 3,11 0.076 1.0629 LIRCINCQK 10 HPV 18 E6 101 3,11 0.16 1.0629 LIRCINCQK 10 HPV 18 E6 101 3,11 0.16 1.0649 LIRCINCQK 10 HPV 18 E6 41 3,11 0.009 1.0649 CIVCPICSQK 10 HPV 16 E6 41 3,11 0.009 1.0651 LIEVEEARK 10 HPV 16 E6 41 3,11 0.001 1.0651 DIILECVYCK 10 HPV <th>90</th> <th>_</th> <th>IILECVYCK</th> <th>٥</th> <th>HPV</th> <th>91</th> <th>33</th> <th>ន</th> <th>3,11</th> <th></th> <th>91000</th> <th>9100</th> <th></th>	90	_	IILECVYCK	٥	HPV	91	33	ន	3,11		91000	9100	
1.0996 CIDFTSRIR 9 HPV 18 E6 68 3,11 0.010 1.0596 GTTLEQQYNK 10 HPV 16 E6 92 3,11 0.010 1.0506 LLIRCLINCQK 10 HPV 18 E6 101 3,11 0.076 1.0529 LLIRCLINCQK 10 HPV 18 E6 101 3,11 0.17 1.0614 LIRCLINCQK 10 HPV 18 E6 41 3,11 0.16 1.0629 CIVCPICSQK 10 HPV 16 E7 88 3,11 0.0009 1.0625 LTEVFEFAFK 10 HPV 16 E6 41 3,11 0.0009 1.0621 JILICCVYCK 10 HPV 16 E6 41 3,11 0.0009 1.1051 KIRHLINEKRR 10 HPV 16 E6 37 3,11 0.001 1.1052 CYYCKQQLIR 10	5		CIDFYSRIR	٥	HPV	. 18	纽	38	3,11		0.017	91000	
1.0696 CTTLEQQYNK 10 HPV 16 E6 92 3,11 0.010 1.0606 LLIRCLINCQK 10 HPV 18 E6 101 3,11 0.076 1.0598 LLIRCLINCQK 10 HPV 16 E6 101 3,11 0.12 1.0629 LLIRCLINCQK 10 HPV 18 E6 41 3,11 0.0009 1.0644 LIEVFEFAFK 10 HPV 16 E7 88 3,11 0.0009 1.0655 LTEVFEFAFK 10 HPV 16 E6 41 3,11 0.0009 1.0657 LTEVFEFAFK 10 HPV 16 E6 41 3,11 0.0009 1.0657 LIEVFEFAFK 10 HPV 16 E6 41 3,11 0.0009 1.1059 LIEVFEFAFK 10 HPV 16 E6 37 3,11 0.0009 1.11054 CVYCKQQLIR 10	Ē		CIDENSRIR	6	HPV	18	33	38	3,11		0.010	00000	
1.0666 LLIRCLRÇQK 10 HPV 18 E6 101 3,11 0.076 1.0586 LLIRCLNCQK 10 HPV 16 E6 101 3,11 0.12 1.0629 LLIRCLRCQK 10 HPV 18 E6 41 3,11 0.06 1.0614 LTEVFEFAFK 10 HPV 16 E7 88 3,11 0.0009 1.0625 LTEVFEFAFK 10 HPV 16 E6 41 3,11 0.0009 1.0621 DIILECVYCK 10 HPV 16 E6 41 3,11 0.0017 1.1059 DIILECVYCK 10 HPV 16 E6 37 3,11 0.0065 1.1103 KLRHLNERRR 10 HPV 16 E6 37 3,11 0.01 1.1103 KURHLUERRR 10 HPV 16 E6 37 3,11 0.01	212		GTTLEQQYNK	2	HPV	16	E6	8	3,11		0.010	88	
1.0596 LLIRCINCQK 10 HPV 16 E6 106 3,11 0,12 1.0629 LLIRCLRCQK 10 HPV 18 E6 41 3,11 0,16 1.0614 LTEVFEFAFK 10 HPV 16 E7 88 3,11 0,0009 1.0625 CIVCPICSQK 10 HPV 16 E6 41 3,11 0,0017 1.0621 DIILECVYCK 10 HPV 16 E6 3,11 0,0012 1.1103 KLRHLNERRR 10 HPV 16 E6 37 3,11 0,0012 1.1103 KURHLNERRR 10 HPV 16 E6 37 3,11 0,0013 1.1103 CVYCKQQLIR 10 HPV 16 E6 37 3,11 0,013	+5+		LLIRCLINCOK	2	HPV	18	93	101	3,11		9200	629	
1.0629 LLIRCLRCQK 10 HPV 18 E6 41 3,11 0.16 1.0614 LTEVFEFAFK 10 HPV 18 E6 41 3,11 0.0009 1.0625 CIVCPICCQK 10 HPV 16 E6 41 3,11 0.0017 1.0625 LTEVFEFAFK 10 HPV 18 E6 41 3,11 0.0017 1.0591 DIILECVYCK 10 HPV 16 E6 32 3,11 0.0065 1.1103 KIRHLNEKRR 10 HPV 18 E6 17 3,11 0.0065 1.1103 CVYCKQQLIR 10 HPV 16 E6 37 3,11 0.013	513		LLIRCINCOK	20	HPV	16	E6	100	3,11		0.12	024	
1.0614 LTEVFEFAFK 10 HPV 18 E6 41 3.11 0.0009 1.0605 GIVCPICSQK 10 HPV 16 E7 88 3.11 0.0017 1.0625 LTEVFEFAFK 10 HPV 18 E6 41 3,11 0.0012 1.0591 DIILECVYCK 10 HPV 16 E6 32 3,11 0.0065 1.1101 KLRHLNEKRR 10 HPV 18 E6 17 3,11 0.013 1.1065 CVYCKQQLIR 10 HPV 16 E6 37 3,11 0.013	##		LLIRCLRCQK	2	HPV	18	93	101	3,11		0.16	0.11	
1.0605 CIVCPICSQK 10 HPV 16 E7 88 3,11 0.0017 1.0625 LTEVFEFAFK 10 HPV 18 E6 41 3,11 0.0012 1.0591 - DIILECVYCK 10 HPV 16 E6 32 3,11 0.0065 1.1101 KLRHLNEKRR 10 HPV 18 E6 117 3,11 0.013 1.1095 CVYCKQQLLR 10 HPV 16 E6 37 3,11 0.011	श्रुद		LTEVFEFAFK	22	HPV	18	E6	#	3,11		0000	0.11	
1.0625 LTEVFEFARK 10 HPV 18 E6 41 3.11 6.0012 1.0591 - DIILECVYCK 10 HPV 16 E6 32 3.11 0.0065 1.1103 KLRHLNEKRR 10 HPV 18 E6 117 3.11 0.013 1.1095 CVYCKQQLLR 10 HFV 16 E6 37 3.11 0.011	215		GIVCPICSQK	2	HPV	. 16	Θ	88	3,11		71000	0900	
1.0591 - DIILECYYCK 10 HPV 16 E6 32 3.11 0.0065 1.1101 KLRHLNEKRR 10 HPV 18 E6 117 3,11 0.013 1.1095 CYYCKQQLLR 10 HPV 16 E6 37 3,11 0.011	5	_	LTEVFEFAFK	2	HPV	18	23	₹	3,11		0.0012	1900	
1.1101 KURHLNEKRR 10 HPV 18 E6 117 3.11 0.0013 1.1095 CVYCKQQLLR 10 HPV 16 E6 37 3.11 0.0011	516		- DIILECYYCK	2	HPV	16	ង	32	3,11		9000	0.021	
1.1095 CVYCKQQLLR 10 HPV 16 E6 37 3,11 0.011	517	1.1101	KLRHLNEKRR	01	НР∨	18	33	11	3,11		0.013	0	
	518	1.1095	CVYCKQQLLR	2	НРУ	91	Ęę	37	3,11		ווייס	0.0059	

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A24	Ш	•		٥																	;										1	ž	9	9200								
A11	60000	90000	20000	\$000 5	۰	8						8	0,000		9200		0000	033	85	917	7500	0000	0,000	6000	3	000	0000	8000	25	A S					22	13	1.0	9670	0.96	0.16	2200	1100
A32	0,0002	0.0006	0	40.000	0	0.0013						€0000¢	40009		40.0009		17.0	0.043	0.31	40.00GB	97000	0.014	0.011	0.0	ક્ર	0.14	0.032	603	A.0003	A 0000	0.18				Ş	0,0093	910:0	0.0002	12	10000	0.14	0000
7	18	66	2.1	1.9	::	0.42	0.099	0.055	0.050	0.043	0.011	2.6	12	0.56	0.17	0.044																	T									
Motif	-	١	-		1	-	-	-	1	1	1	1	1	1	1	1	3	3	3	9	3	3	9	3	9	c			-	~	F	\$ 2	7.	72	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
P.	191	191	240	161	191	,243	273	6	4	6	128	9	529	1/12	8	252	£	99	Z	239	98	229	4	230	107	æ	242	283	812	ž	R:	2 5	3 2	28	8	ŝ	38	62	8	2	128	182
Molecule							Mau							Mai			The V		ASU		MULL			NJU			Mail	INEW			Ě			Ě								
Strain	٣	5/51	1	9	1	1	1	3	3	2	1	3	1	1	2	-	-	1	1	1	. 1	1	1	1	1	1	-	-	-	1	-	,		1	1	-	r	1	1	-		1/3
Virus	MAGE	MAGE	MACE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	WAS:	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE	MAGE
¥	•	٥	0	6	6	6	٥	۵	۵	۵	6	2	2	2	2	2	۵	۵	۵	6	٥	6	6	01	2	2	10	2	2	2	۽ ا	۰ ۱	2 2	2	•	۵	6	۵	2	2	2	01
Sequence	EVDPICHLY	EADPTSNTY	TODLVQEKY	EVDPICHVY	EADPTICHEY	LWEKNEY	TSYMKVLEY	SALPTIMENY	CSVVCNWQY	SSESTTINY	MLESVEONY	ASSLPTTMENY	LTQDEVQERY	EISYVICHLEY	ASSETTINY	DILVOERCALEY	TSYNKWLBY	TITALITICAL	ALAETSYVK	LIGOLVQEK	LVQERYLEY	HEAYCEPRK	LFRAVITICK	KVKHFFSLR	ADLVCFLLLK	ESLFRAVIIK	DLWGERMEN	YVEVSAEVE	LSVMEVYDGR	KAEMLESVIK	KALAETSYVK	NIPLWX SI	LYPATOLG	SYMKMERYI	SLFRAVITK	SYMENTOGR	TITNIFIROR	LTQDLVQEK	SLFRAVITICK	LITOOLVQEK	MLESVIDOYYK	LICONODAPK
Peptide		3.0172	ŀ	3.0173				20009	11002	20008	ı	! 1	20167		ı		990079		190079		,			1 1			61109		- 1	- 1		200010			ł		1,1004		1,0634	1,0607	1,0640	19971
SEQ 10	5	8	Ē	Z,	8	G	585	25	Ġ	528	B	8	R	S	S	K	(3)	535	936	th	766	33	B	2	舌	245	534	543	545	245	2	5	, 5	99	18	252	235	\$	83	6	235	S

added

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			Table 22(i))										
A24		0												
A11	0.029	0.049	0.0020	0.73	1.1	0.095	0.091	0.0052	0.0080	0.88	0.0017	0.054	0.011	0.0006
A3.2	0.0010	6,023	0.0014	1.5	0.46	00000	0.0015	0.020	33	2.6	0.099	0.0005	a.014	0.013
14	29.5	0.33	0.022											
Motif	-	-	-	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11	3,11
Pos.	977	117	<u>8</u>	156	124	31	283	333	83	101	177	311	B	187
Molecule Pos. Motif														,
Strain														
Virus	p53	p53	p53	p53	p53	SZ4	83	554	82	82	192	EŞd.	ESq.	65q
₩₩	6	2	2	6	6	0	9	6	2	2	2	92	2	2
Sequence	сѕрстпну	GTAKSVTCTY	RVEGNLRVEY	RVRAMAIYK	CTYSPALNK	NTSSSPQPK	RTEEENLRK	ELNEALELK	RTEEENLRKK	KTYQCSYCFR	WRRCPHINER	NTSSSPQPKK	RVCACPCRDR	GLAPPQHLIR
Peptide	1.0281	1.0667	1.0672	1.0278	1.0276	1.0285	1.0284	1.0287	1.0678	1.1113	1.1115	1.0679	1.1121	1.1116

						j	19be 2									
A24	0	0	0	0	0	0	0.0022					2.5	0.44	0.11	0.032	0.024
A11	0.0002	0.0002	0.055	0.0002	0.0004	0.0004	0.0024	0.089	0.12	12	a.014					
A3.2	<0.0002	<0.0002	<0.0002	<0.0002	0.0026	0,0005	0.015	0.0057	0.056	0.10	<0.0004			,		
A1	3.4	0.78	0.77	960'0	14	12	0.62	0.018								
Motif	-	-	-	-	-	1	1	-	3	Ξ	11	24	24	74	24	24
Pos.	322	18	311	35	82	82	R	322	263	274	13	318	213	83	302	30
Molecule																
Strain																
Virus	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP	PAP
*	٥	6	6	6	2	2	2	2	2	٥	2	۵	0	۵	6	10
Sequence	KGEYFVEMY	LGEYIRKRY	ASCHLTELY	ESYKHEOWY	LSEISLISLY	LSELSLISLY	LTQLGMEQHY	KGEYFVEMYY	LVNEILNHMK	ATQIPSYKK	ETLKSEERQK	LYFEKGEYF	LYCESVHINF	PYKDFIATL	VYNGLLPPY	PYASCHLTEL
Peptide	3.0175	3.0174	3.0166	3.0163	3.0027	3.0025	3.0236	3.0238	3.0230	3.0158	3.0231	3.0161	3.0160	3.0159	3.0162	3.0232

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added (

Table 23(k)

Peptidel	Sequence	(SERID)	MA	Virus	Strain	Molecule	Pos.	Motif	_A1	A3.2	λ11	Aze
1.0000	ALPERPSLY	(587)	9 1	PSA			231	1	0.011			
20157	VSHSFPHPL	Y SPA	10	F5A			-	1	0.15	<0.0003	0.0015	
1.0245	PLYDMSLL	K (539)	9	PSA		İ	15	3.11		0.24	0.007	
1.0273	VVHYRKWI		•	PSA			242	3.11		0.0072	0.093	
1.0002	YTKVVHYR		,	PSA	i		229	3.11		0.0006	0.058	
1.1009	SLUKNREL		,	P5A			100	3.11		0.0004	0.047	
1.0250 I	IVCCMBCE	X(593)	•	PSA			71	3.11		0.041	0.019	
1.0249	QVHPQKVT	X(594	9	PSA	:	7	142	3,11		0.0060	0.014	
1.1112	SLYTKVVH	YRV595	10	P5A			237	3.11		0.28	0.23	
1.0653	LTAAHOR	1K/546	10	PSA			57	3,11		0.14	0.083	
1.0651	RIVECWEC			P5A			20	3,11		0.044	0.067	
1.0642	KVVHYIUKW	TKY57	10	PSA			241	3.11		0.045	0.045	
1.1111	VTKPMLCA			PSA			1#	3,11		0.0003	0.012	
3.0106 1	MLLRLSEP	A (600	1	PSA			118	Random				
			\top	ddea	1							

TABLE 24: CTL EPITOPES IDENTIFIED IN PEPTIDE SCREENING.

Sequence	Antigen	Motif	Id
EVDPIGHLY	MAGE3	A01	1044.07
ASSLPTTMNY	MAGE3	A01	1044.01
EADPTGHSY	MAGE1	A01	958.01
SSLPTTMNY*	MAGE3	A01	1072.02*
GSVVGNWQY*	MAGE3	A01	1072.03*
ALAETSYVK*	MAGEIN	A03	1072.38*
SLFRAVITK	MAGE1	A11	1072.13
RALAETSYVK	MAGEIN	A11	1072.39
ESLFRAVITK	MAGE1	A11	1072.15
KVYLAWVPAHK	HIV	A3/11*	1069.42*
TVYYGVPVWK	HIV	A03	1069.43
KLAGRWPVK	HIV	A03	1069.44
KMIGGIGGFIK	НΙΥ	A03	1069.45
AIFQSSMTK	HIV	A03	966.01
WTYQIYQEPFK	НΙ	A03	1069.46
FLGKIWPSHK*	HIV	A03	1069.56*
TVYYGVPVWK	HIV	A11	1052.03
VTVYYGVPVWK	НΙΥ	A11	1069.47
GVAGALVAFK	HCV	A03	1073.10
CTCGSSDLY	HCV	A11	1069.62
GVAGALVAFK	HCV	A11	1052.05
LLDTASALY*	HBV	A01	1069.01*
TLWKAGILYK	HBV	A03	1069.15
 borderline po: 	sitive		·

Version with markings to show changes made

	i	1					
		Table 25 a					
		Peptides Syntl	nesized				
		by Cytel For Loading					
5		Onto Acid Stri	pped				
		Autologous PBM	Cs and				
		PHA Blasts	(SEQ ID)				
	Peptide ID #	Antigen (No: Sequence				
	777.03	HBs	(606) FLLTRILTI				
10	924.07	HBc	(607) FLPSDFFPSV				
	927.32	НВр	(608) GLYSSTVPV				
	938.01	MAGE 1	(523) EADPTGHSY				
	939.03	PSA	(609) VLVHPQWVL				
	941.01	HBc	(610) FLPSDYFPSV				
15	1044.04	PAP	(611) ILLWDPIPV				
	1044.05	PSA	(615) KTOCADTAHI				
	1044.06	PSA	(6/3) MLLRLSEPAEL				
			added				
20	Table 25 b						
	Cell Population	125I-Labeled	CPMS				
		Peptide +/- C	old +/- std. dev.				

Peptide

- cold peptide

+ cold peptide

-cold peptide

+ cold peptide

3553 ± 157

370 ± 37

50

n = 3

n = 1

JY acid stripped

25 JY acid stripped

JY control

JY control

TABLE 13 VALIDATION OF CYTEL'S HLA MOTIFS

	Bir	nding Cap	pacity (IC	50 ^{nM)}		
Sequence	Motif	A1	A2.1	A3.2	A11	A24
AADKAAAAY	Al	50	*	••		
ATAKAAAAY	A1	15		329	77	·.
ATDKAAAAY	A1	2.8		9250	840	ND
ALAKAAAAV	A2.1		125			
AMAAAAAAK	A3.2			48	8.4	
АТАЛАЛАЛАК	A11			59	40	
AYAKAAAAF	A24		••	• •	••	115

15 *A dash indicates an IC₅₀ greater than 20,000 nM.

TABLE 14 VALIDATION OF CYTEL'S HLA MOTIFS

	8	inding Capac	ity (IC ₅₀ nM)		
SEQUENCE	MOTIF	Al	A2.1	A3.2	A11
AADKAAAAY	. A1	45	•••	••	••
ATAKAAAAAY	A1	58		1100	1030
ATDKAAAAAY	Al	4.0		10000	4533
ALAKAAAAAV	A2.1	ND	1400	••	
AMAAAAAAK	A3.2	ND		85	24.0
ATAAAAAAAK	A11		• •	216	88

*A dash indicates an IC_{50} greater than 20,000 nM.





HLA-A3.2

PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION
952.25	ALAAAAAAK	1	•
952.26	АМААААААК	1.2	position 2
952.23	AVAAAAAAK	0.95	
981.04	ASAAAAAAK	0.89	
952.24	AIAAAAAAK	0.57	
952.27	AAAAAAAAK	0.57	
981.06	ATAAAAAAK	0.49	
981.08	AFAAAAAAK	0.13	
981.09	AGAAAAAAK	0.077	
981.13	ACAAAAAAK	0.031	
981.12	ADAAAAAK	0.014	
981.11	ANAAAAAAK	0.0010	
981.05	AKAAAAAAK	<0.0016	
981.07	AYAAAAAAK	<0.0005	
981.10	APAAAAAAK	<0.0006	
952.35	ALAAAAAAR	0.46	position 9
981.36	ALAAAAAAY	0.15	
981.33	ALAAAAAA	0.0034	
981.35	ALAAAAAAQ	<0.0006	
981.37	ALAAAAAAS	<0.0005	
981.38	ALAAAAAAT	<0.0005	
981.34	ALAAAAAAN	<0.0005	

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TABLE 16

HLA-A11

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION
	952.25	ALAAAAAAK	1	
	952.26	AMAAAAAAK	2.5	position 2
	952.27	AAAAAAAAK	1.1	
	952.24	AIAAAAAAK	0.72	
10	981.06	АТАААААА	0.55	
	981.04	ASAAAAAK	0.46	
	981.09	AGAAAAAAK	0.38	
	952.23	AVAAAAAAK	0.23	-
	981.11	ANAAAAAAK	0.23	
15	981.13	ACAAAAAAK	0.019	
	981.08	AFAAAAAAK	0.020	
	981.12	ADAAAAAAK	0.012	
	981.05	AKAAAAAAK	0.0065	
	981.07	АУАЛАЛАЛ	<0.0065	
20	981.10	АРАЛАЛАЛ	<0.0051	
;	952.35	ALAAAAAAR	0.015	position 9
	981.33	ALAAAAAA	<0.0059	
İ	981.34	ALAAAAAAN	<0.0071	·
	981.35	ALAAAAAQ	<0.0051	
25	981.36	ALAAAAAAY	<0.0071	
	981.37	ALAAAAAAS	<0.0051	
	981.38	ALAAAAAAT	<0.0051	
	981.39	ALAAAAAAE	<0.0071	
	10	952.25 952.26 952.27 952.24 10 981.06 981.04 981.09 952.23 981.11 15 981.13 981.08 981.12 981.05 981.07 20 981.10 952.35 981.33 981.34 981.35 981.36 981.37 981.38	952.25 ALAAAAAK 952.26 AMAAAAAK 952.27 AAAAAAAK 952.24 ALAAAAAK 952.24 ALAAAAAK 981.06 ATAAAAAK 981.09 AGAAAAAK 981.09 AGAAAAAK 981.11 ANAAAAAK 981.11 ANAAAAAK 981.12 ADAAAAAK 981.12 ADAAAAAK 981.05 AKAAAAAK 981.07 AYAAAAAK 981.07 AYAAAAAK 981.07 AYAAAAAK 981.30 ALAAAAAK 981.31 ALAAAAAA 981.33 ALAAAAAA 981.33 ALAAAAAA 981.34 ALAAAAAA 981.35 ALAAAAAA 981.36 ALAAAAAAY 981.37 ALAAAAAA	952.25 ALAAAAAK 1 952.26 AMAAAAAAK 2.5 952.27 AAAAAAAK 1.1 952.24 ALAAAAAAK 0.72 10 981.06 ATAAAAAAK 0.55 981.04 ASAAAAAAK 0.46 981.09 AGAAAAAAK 0.46 981.09 AGAAAAAAK 0.38 952.23 AVAAAAAAK 0.23 981.11 ANAAAAAK 0.23 981.11 ANAAAAAK 0.019 981.08 AFAAAAAAK 0.019 981.08 AFAAAAAAK 0.012 981.12 ADAAAAAAK 0.012 981.05 AKAAAAAAK 0.012 981.07 AYAAAAAAK 0.0055 981.07 AYAAAAAAK 0.0055 981.33 ALAAAAAAK 0.0059 981.34 ALAAAAAA 0.0059 981.35 ALAAAAAAA 0.0071 981.35 ALAAAAAAA 0.0071 981.36 ALAAAAAAY 0.0071 981.37 ALAAAAAAY 0.0051

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TABLE 17

HLA-A24

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PEPTIDE	SEQUENCE	AVERAGE RATIO TO 983.01	SUBSTITUTION
983.01	AYAKAAAAF	. 1	•
983.08	AFAKAAAAF	0.24	position 2
983.09	APAKAAAAF	0.0058	
983.10	AAAKAAAAF	0.0023	
983.11	AKAKAAAAF	<0.0012	
983.05	AYAKAAAAI	0.20	position 9
983.04	AYAKAAAAL	0.11	
983.06	AYAKAAAAV	0.0023	
983.02	АЧАКААААА	<0.0012	
983.03	АУАКАААА	<0.0012	
983.07	AYAKAAAAK	<0.0012	

TABLE 18

HLA-A1

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION
	982.011	ATDKAAAAY	Motif	
	982.07	ATAKAAAAY	1	-
	982.09	ASAKAAAAY	0.17	position 2
	982.13	AMAKAAAAY	0.095	no D in pos 3
10	982.08	АААКАААА	0.0064	
	954.09	ALAKAAAAY	0.0045	
	954.11	AIAKAAAAY	0.0045	
	954.13	AVAKAAAAY	0.0020	
	982.10	АКАКАААА	0.0011	
15	982.11	ANAKAAAAY	<0.0001	
	982.12	ADAKAAAAY	<0.0001	
	982.14	AGAKAAAAY	<0.0001	
	982.15	АРАКАААА	<0.0001	
	982.16	АУАКААААУ	<0.0001	
20	982.17	AHAKAAAAY	<0.0001	
	982.24	АТАКААААА	0.0040	position 9
	982.23	ATAKAAAAF	0.0019	no D in pos 3
	982.28	Атакаааан	0.0010	
	982.32	ATAKAAAAV	0.0005	
25	982.25	ATAKAAAAN	<0.0001	
	982.26	ATAKAAAAD	<0.0001	
	982.27	ATAKAAAAW	<0.0001	
	982.30	АТАКААААК	<0.0001	
	982.31	ATAKAAAAI	<0.0001	
30	982.29	АТАКААААР	<0.0001	•



TABLE 19

HLA-A1

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION
	982.01	ATDKAAAAY	Motif	
	982.07	АТАКАААА	1	
	982.01	AADKAAAAY	0.14	position 3
	954.03	AAEKAAAAY	0.038	no T in pos 2
10	982.02	AAAKAAAAY	0.0055	
	982.06	AASKAAAAY	0.0024	
	982.04	AANKAAAAY	0.0011	
	982.03	AAQKAAAAY	0.0008	
	982.05	AAKKAAAAY	<0.0001	
15	982.20	AADKAAAAA	0.0016	position 9
	982.21	AADKAAAAW	0.0005	no T in pos 2
	982.19	AADKAAAAF	<0.0001	-
	982.22	AADKAAAAK	<0.0001	



TABLE 20(A)

HPV16 E6 AND E7 PEPTIDES BINDING TO HLA-A1

5	Orgin	First aa Position	Sequence*	Binding Ratio to Standard:	Motif Prediction
	E6	80	ISEYRHYAY	3.500	+
	B6	69	VADKALKFY	0.240	•
	B7	44	QAEPDRAHY	0.029	•
10	E7	37	EIDGPAGQA	0.025	-
	E7	19	TTDLYAYEQ	0.023	•
	E6	144	MSAARSSRT	0.019	+/-
	E7	73	HVDIRTLED	0.014	-
	E6	139	WTGRAMSAA	0.010	•
15	E6	61	YRDGNPYAV	0.008	•

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC_{50} value $\pm SE$ of the standard in the course of the experiments considered in this table was 81±30 nM. Listed in the table are peptides yielding ratio values of ≥0.001. All other peptides yielded ratio values of ≤0.001.

TABLE 20 (B)
HPV16 E6 and E7 Peptides Binding to HLA-A3.2

5	Origin	First aa Position	Sequence*	Binding Ratio to Standard:	Motif Prediction
	E6	107	LIRAINAQK	3.7000	+
	E6	59	IVYRDGNPY	3.0000	•
	E7	89	IVAPIASQK	2.2000	•
10	E6	33	IILEAVYAK	1.5000	•
	E6	125	HLDKKQRFH	0.4400	•
	E6	143	AMSAA RSSR	0.1800	•
	E6	. 7	AMFQDPQER	0.1000	•
	E6	93	TTLEQQYNK	0.0780	•
15	E6	37	AVYAKQQLL	0.0320	-
	E7	51	HYNIVTFAA	0.0210	-
	E6	145	SAARSSRTR	0.0200	• -
TE E	E6	75	KFYSKISEY	0.0100	+
<u>T</u> ♣	E6	89	SLYGTTLEQ	0.0080	•
20	E7	52	YNIVTFAAK	0.0067	•
	E6	80	ISEYRHYAY	0.0064	•
	E6	42	QQLLRREVY	0.0058	-
	E6	68	AVADKALKF	0.0056	•
tank tank tank	E6	97	QQYNKPL A D	0.0045	•
25	E6	79	KISEYRHYA	0.0044	•
	E6	84	RHYAYSLYG	0.0036	-
	E6	69	VADKALKFY	0.0025	•
	E6	146	AARSSRTRR	0.0020	•
	E7	58	AAKADSTLR	0.0016	+
30	E6	38	VYAKQQLLR	0.0012	-
	E6	67	YAVADKALK	0.0012	+
	E7 .	60	KADSTLRLA	0.0012	_

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 30±3 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of ≤0.001.



Table 20(C) HPV16 E6 and E7 Peptides Binding to HLA-A11.2

	5	Orgin	First aa Position	Sequence*	Binding Ratio to Standard:	Motif Prediction
		E6	33	IILEAVYAK	6.7000	+
		E6	93	TTLEQQYNK	1.8000	•
		E7	89	IVAPIASQK	1.3000	+
	10	E6	7	AMFQDPQER	0.8400	+/-
		B6	59	IVYRDGNPY	0.4700	- (+) S
		E6	80	ISEYRHYAY	0.4300	- (+) 5
		E6.	37	AVYAKQQLL	0.0450	•
		E6	145	SAARSSRTR	0.0330	+/-
	15	E6	107	LIRAINAQK	0.0120	•
		E7	58	AAKADSTLR	0.0110	+/-
		E6	42	QQLLRREVY	0.0084	+/- (+) 5
ui Ui		E6	143	AMSAARSSR	0.0084	•
UT.		E6	79	KISEYRHYA	0.0076	-
	20	E6	67	YAVADKALK	0.0074	+
H		E7	52	YNIVTFAAK	0.0060	•
		E6	68	AVADKALKF	0.0037	-
		E6	69	VADKALKFY	0.0030	- (+) 5
		E6	38	VYAKQQLLR	0.0022	+/-
	25	E6	140	TGRAMSAAR	0.0012	+/-
		E7	90	Vapiasokp	0.0012	-
		E7	51	HYNIVTFAA	0.0010	

Bold A's indicate residues in which cysteine was replaced by alanine.

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 10±3 nM. Listed in the table are peptides yielding ratio value of ≥ 0.001 . All other peptides yielded ratio values of ≤ 0.001 . Brackets indicate score according to adjusted motif.





Table 20(D) HPV16 E6 and E7 Peptides Binding to HLA-A24

5	Orgin	First aa Position	Sequence*	Binding Ratio to Standard:	Motif Prediction
	E6	87	AYSLYGTTL	0.1200	•
	E6	72	KALKFYSKI	0.1100	- (+)5
	E6	131	RFHNIRGRW	0.1000	+
0	87	49	RAHYNIVTF	0.0670	- (+)\$
	26	49	VYDFAFRDL	0.0610	•
	B6	82	EYRHYAYSL	0.0460	•
	B6	26	LQTTIHDII	0.0200	•
	B6	66	PYAVADKAL	0.0055	•
5	E6	1	MHQKRTAMF	0.0049	-
	E6	85	HYAYSLYGT	0.0037	-
	E6	44	LLRREVYDF	0.0023	•
-	E6	38	VYAKQQLLR	0.0011	±

Bold A's indicate residues in which cysteine was replaced by alanine.

20

The average IC₅₀ value $_1SE$ of the standard in the course of the experiments considered in this table was 22 $_16$ nM. Listed in the table are peptides yielding ratio value of $_10.001$. All other peptides yielded ratio values of $_10.001$. Brackets indicate score according to adjusted motif.

aft.

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For HLA-A11 (A*1101):

- 1 XTXXXXXXX
- 2 XTXXXXXXXX
- 3 XVXXXXXXX
- 4 XVXXXXXXXX

For HLA-A24.1 (A*2401):

- 1 XYXXXXXXF
- 2 XYXXXXXXXF
- 3 XYXXXXXXL
- 4 XYXXXXXXXL

Peptides with MHC Class I Binding Motifs Table 9

	4	• •	•	
	AA Position	Sequence	Antigen	HLA molecule
		30 IHDIILECVY	HPV16.E6	A1
		69 VCDKCLKFY	HPV16.E6	A1
5		77 YSKISEYRHY	HPV16.E6	A1
		80 ISEYRHYCY	HPV16.E6	A1
		92 GTTLEQQYNK	HPV16.E6	A11
		93 TTLEQQYNK	HPV16.E6	A11
		106 LLIRCINCQK	HPV16.E6	А3
10				
		2 HGDTPTLHEY	HPV16.E7	A1
		16 QPETTDLYCY	HPV16.E7	A1
		44 QAEPDRAHY	HPV16.E7	· A1
		89 IVCPICSQK	HPV16.E7	A3, A11
<u>4</u> 15				
		3 RFEDPTRRPY	HPV18.E6	A1
15 II II II II II II II II II II II II II		4 FEDPTRRPY	HPV18.E6	A1
		25 LQDIEITCVY	HPV18.E6	A1
		41 LTEVFEFAFK	HPV18.E6	A11
a 20		72 YSRIRELRHY	HPV18.E6	A1
J		84 SVYGDTLEK	HPV18.E6	A3, A11
		101 LLIRCLRCQK	HPV18.E6	A3
14		59 HTMLCMCCK	HPV18.E7	A11
25				

Human Papilloma Virus 16 and 18 (E6 and E7 Proteins)



Peptides with MHC Class I Binding Motifs Table 10

	AA Position	Sequence	Antigen	HLA molecule
5		2 SLEQRSLHCK	MAGE 1	A3
		96 SLFRAVITK	MAGE 1	А3
		96 SLFRAVITKK	MAGE 1	А3
		108 DLVGFLLLK	MAGE 1	A3
		128 MLESVIKNYK	MAGE 1	A3
10		128 MLESVIKNY	MAGE 1	A1
		152 QLVFGIDVK	MAGE 1	A3
		161 EADPTGHSY	MAGE 1	A1
		182 LLGDNQIMPK	MAGE 1	A3
new.		215 WEELSVMEVY	MAGE 1	A1
1 5 0 0 0 0 0 0 0 0 0 0		223 VYDGREHSAY	MAGE 1	A1
Ī		238 LLTQDLVQEK	MAGE 1	A3
		239 LTQDLVQEK	MAGE 1	A11
		239 LTQDLVQEKY	MAGE 1	A1
□ □ □ 20		240 TQDLVQEKY	MAGE 1	A1
<u> </u>				

Melanoma Antigen MAGE 1



Peptides	with	MHC	Class	I	Binding	Motifs	Table	11
						-		

	AA Position	Sequence	Antigen	HLA molecule
5		21 IVGGWECEK	PSA	A3, A11
		57 LTAAHCIRNK	PSA	A11
		88 VSHSFPHPLY	PSA	A1
		95 PLYDMSLLK	PSA	A 3
		178 DVCAQVHPQK	PSA	A3, A11
10		182 QVHPQKVTK	PSA	A3, A11
		236 PSLYTKVVHY	PSA	A1
		239 YTKVVHYRK	PSA	A11
		241 KVVHYRKWIK	PSA .	A3, A11
		242 VVHYRKWIK	PSA	A3, A11
15				•

Prostate Specific Antigen (PSA)

nacestro netano



Sequence

2 STNPKPQRK 14 NTNRRPQDVK **43 RLGVRATRK** 302 VQDCNCSIY 556 WMNSTGFTK

605 LTPRCMVDY 626 FTIFKIRMY

AA Position



Peptides with MHC Class I Binding Motifs

Antigen	HLA molecule
нсч	A11
HCV	A11
HCV	A3
HCV	A1
HCV	A3
HCV	λ1

A1

Table 12

Hepatitis C Virus (Consensus Sequence)

HCV

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				103	<u>, </u>	_					
Peptide	Sequence	*	Virus	Strain	Molecule	Pos.	Motif	Al	A32	All	AZI
1,0000	HLDMLRHLY	9	CEREZ			Q	1	9.1	0.007	0.0002	~
1.0346	LLDODETEY	9	CERRO			140	1	7.6	0.0003	0	
1,0305	CTOLFEDNY	•	CEREZ		<u> </u>	104	1	0.18	0	0.028	
1,0065	LTCSPOREY	1 9	CERRO			1131	1	0.13	-	0.0051	
1.0017	ETLEBICY	,	CERB2			401	1	0.043	<u> </u>	-	
1.0749	PTHOSOVWSY	10	CERUIZ			899	1	2.7	0.0003	0.0005	
1.0747	RLLDIDETEY	10	CERB2			868	1	1.3	0.0017	0	
1.0715	TLEETCYLY	10	CERB2			402	1	1.1	0		
1.0737	YVMAGVCSPY	10	CEREZ			772	- i -	1.1	0.010	0.012	0
1.0764	CIPTAENPEY	10	CERB2			1239	1	0.063		0.012	
1,0706	LIORNIPOLCY	10	CERIEZ			154	i	0.000			
1.0663	VVOCNLELTY	10	CEREZ			55	-	0.018			
1.0754	MCDLVDAEEY	10	CERBO			1014		0.012			
1.1028	KIRKYTMER	1	CERB2			451	3,11		0.76	0.0018	
1.1027	VVPCILIKIX	1	CERIE			449	3.11		0.11	0.72	
1.0344	LVKSPNHVK	-	CERRO			452	3.11		0.48	0.070	
1,0005	VURENTSPK	1 5	C-EREZ			754	3.11		0.40	0.013	
1,0329	ILIKUUROOK	9	derez			673	3.11		0.34	0.0097	
1,0311	ILWIKDIFHIK	9	CERT			167	3.11		0.78	0.37	
1,1033	KITOPCLAR	•	CERCIE2			240	3.11		0.17	0.34	
1000	GVVFCILIK	-	C-EXEX				3.11		0.0067	0.000	
1.0299	QVCTGTDMK	-	CERTS			24	3.11		0.0007	0.052	
1.1031	LLOHVRENR	9	C-EREZ			106	3.11		0.037	40,000	
1.1026	CVNCSOFLE	1 5	CERUS2	\		528	111		0.0015	0.031	
1,1023	TVCACCCAR	9	C-EREZ	_		218	3.11		0.0004	0.031	
1,0331	ILKETELEK	9	C-EREZ			714	111		0.019	0.0023	
1.1024	VIAEDCTOR	9	C-ERIZ			322	3.11		<0.0000	0.014	
1,006 1	OLSYMPTWK	9 1	CEREZ			607	111		0.0005	0.014	
1.0707	TILWKDIFHK	10	C-EREZ	$\overline{}$		166	3.11		0.043	14	
1,0712 1	CTORCEXCSK	10	CEREZ			327	3.11		0.021		
1,0736	KYLRENTSPK	10	CEREZ		\	753	3.11		0.38	0.61	
1.0702	OURSLITETLK	10	C-ERIEZ		_	10	3.11		0.20		
1.110	RLVHRDLAAR	10	c-EBUB2			840	3.11			0.013	
1.0741	LLNWONQLAK	10	CERUSO			22	3.11		0.18	0	
1.0752	TIDVYMBAVK	10	C-EAGE2			946	311		0.14	0.14	
1,0731	RILKETELIK	10	~EEE2			75	3.11		0.057	0.12	
1.0745	VLVKSPNHVK	10	CERTEZ			201	3.11		0.082	0.0072	
1.1131	SVFONLOVIR	10	CERTS			43	3.11		0.017	0.0073	
1.1133	HTVPWDQLFR	10	C-ERSZ			478	3.11		0.0036	0.027	
1.1127	ILKCCVLIOR	. 10	C-ERB2			148	3.11		0.040	0.0005	
1.1143	LVSEFSRMAR	10	c-ERB2			972	3.11		0.0072	0.033	
1.1136	CVVFCILIKE	10	c-ERB2			449	3.11		0.018	0.033	
1.0726	CVARCESCVK	10	C-ERB2			5%	3.11		0.022	0.0002	
1.1137	VVPCILIKRE	10	c-ERB2			44	3.11		0.0030		
1.0728 1	CILIKRROOK	10	C-EREZ			672	3.11		0.015	0.016	
1.1129	RTVCACCCAR					217				0.0014	
1.1134	GLACHOLGAR	10	CERB2			508	3,11	-	0.0068	0.013	
1.11.04	_ CONTRACTOR N	10	c-ERB2		1		3,11		0.011	1 0 1	

Table 23(a)

:104 IAA Peptide Virus Strain Molecule | Pos. | Motif A1 ATT I A24 1.0291 VCEADYFEY EBNAI 409 I 1 0.016 PLRESIVCY EBNAL 553 0.010 1.0681 PYCEADYFEY 10 EBNAI 408 0.015 1.0683 CTWVACVEVY 10 EBNAI 0.014 1.0293 CVFVYCCSK • EBNAI 506 3.11 1.1016 KTSLYNLER • 514 3.11 EBNAI 0.31 0.12 **AIKDLYMTK** 1.0297 • EBNAI 570 3.11 0.048 0.034 1.0667 **QTHIPAEVLK** EBNAI 547 3.11 0.010 0.21 CTALAIPOCK 10 EBNAT 523 3.11 0.0028

Table 23(b)

				·			.				
		1 1	•	pt .	1	1 /	:		}]	_
Peptide	Sequence	1	Virus	Strain	Molecule	Pos	.Aotif	A1	ALZ	AII	A24
5.0005	CTELKLSDY	: 9 /	กม	A	NP	- 44	1	3.6			
5.0006	STUELISKY	1 9 1	PLU	A	NP	377	1	0.020			
5.0044	ILROSVAHK	9 1	PLU	A	NP	245	3		15	0.0037	
5.0051	RMONILKOK	9 1	FW	A	NP	221	3		0.27	0.062	
5.0046	LMQCSTLITE	191	FLU	A	NP	166	3		0.031	0.10	
5.0048	MIDGIGREY	791	FLU	A	NP	72	3		0.059	0.0010	
5.0049	MVLSAFDER	9.1	PLU	A	NP	"	3		0.00714	0.041	
5.0054	YIQMCTELK	9	FLU	A	NP	40	3		0.0033	0.000	
5.0042	CINDRNEWE	91	กบ	A _	NP	200	3		0.0028	0.024	
5.0104	SUMQCSTLPR	10 1	FLU	Α	NP	145	3		0.12	0.84	
5.0095	KMIDGIGRIY	10	FLU	A	NP	31	3		0.50	0.0079	
5.0096 1	LILECSVAHK	10 1	FLU	A	NP	264	3		0.36	0.007	
5.0102	RSGAAGAAVK	10	FLU	A	NP	175	3		0.019	0.0046	
5.0105	SSTLELISKY	10	FLU	A	NP	376	3		0.0018	0.016	
5.0103	RSKYWAJRTE	10	FLU	A	NP	342	3		0.012	0	
5.0101	RMVLSAFDER	10 1	FLU	A	NP	45	3		0.0014	0.010	
5.0061	FYIQMCTEL.	1	FLU	A	NP	39	24				2.9
5.0060 I	AYERMONIL	1	FLU	A	NP	218	24				0.031
5.0112	REYIQMCTEL	10 1	FLU	A	NP	35	24				0.15

Table 23(c)

- 1		1 1		'							Ì
eptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Aotif	A1	A32	A11	1 42
1.0155 1	LLDTASALY	9	HBV	edf	CORE	420	1	25	0.0007	0	
.0186	SLOVSAAFY	,	HBV	adr	POL	1001	1	17.2	0.0007	0.0006	
2.01.25	PTTCKTSLY	. 9	HBV	ALL	Ī	1,342	1	1.3	0.0008	0	
2.0126	MSTTDLEAY	9	HBV	adr	i	1,521	1	0.85	<0.0008	0	
.0206	PITCRISLY	9	HBV	adr	POL	1362	1	לבס	0	0	
.0367	LTKOYLNLY	9	Hav	=4=	POL	1290	1	0.50	0.0003	0.0075	
20122	LTKQYLNLY	9	HBV	ad w		1,250	1	0.095			
1.0166	KVCNFTCLY	9	HBV	adr	POL	629	1	0.068			
2.0127	MSPTDLEAY	9	HBV	ad w	i	1,550	11	0.067			
2.0120	PSQFSRCINY	9	HBV	ay w		984	1	0.057			
20112	PSEWAFAKY	9	HSV	ad w		316	1	0.054			
20119	QSAVRKEAY	9	HBV	adw		861	1	0.025			
.0174	PLDKGIKPY	1 9 1	HBV	adr	POL	698	1	0.019			
.0378	SMILLYKTY	9	HBV	14	POL	1092	_1_	0.017			
2.0115	ASRDLVVSY	191	HSV	4700	<u> </u>	499	1	0.013			
2.01.24	PSRCRUCLY	9	Hev	adr/adw		1,364	1	0.011			
20121	SSTSKNINY	9	HSV	adr		1,036	1	0.0097			
1.0519	DULDTASALY	10	HBV	ade	CORE	419	1	11.1	0	0	
1.0513	LLDPRVRCLY	10	Hav	adr	ENV	120		43	0.17	0	
2,0239	LSLDVSAAFY	10	HBV	ALL.	POL.	1,000	1	42	<0.000€	0.00327	
1.0911	PLOQUYLHLY	10	HBV	adr	POL	1097	1	1.1	0.074	0.0048	0.00
20016		10	HSV	ayw	- FOR	1.098		0.40	0.0056	0.012	
2.0244	KTYCKKLHLY	10	Hav	ate ate	POL	1098		0.57	0.59	0.22	0 8
2.0242	OTPCRACHLY	10	HBV		 	1.057	1	0.37	0.002	0.011	480
0556	KTFCKCHLY	10	HBV	ayw	POL	1060	-;-	0.34	0.094	0.000	-
2.0041	KTPGRICHLY	10	HBV	adr		1.00	i	0.30	0.15	0.095	- 0
1.0766	LOOPRVRALY	10	HBV	24	ENV	120	i	0.21	0.014	0	
1.0806	TTPAQCTSMY	10	HBV	20	ENV	228	1	0.20	0	-	
2.0240	LSSTSRNINY	10	HBV	adr		1,035	1	0.20	<0.000	-	
1.0541	PLDKCDXPYY	10	HBV	adr	POL	698	1	0.16	0	-	
2.0738	HSASPCCSPY	10	HSV	2700		767	-	0.15	0.019	0.017	0
1.0795	FLTKOYLNLY	10	HBV	adw	POL	1279	1	0.12	0	0	
2 0277	RSASPCCSPY	10	HSV	adr/adw	1	738	1	0.11	0.033	0.020	. 0
1.0074	WLWCMDIDPY	10	HBV	ed w	CORE	416	-i	0.081			-
2.0233	TTPAQCTSMY	10	Hav	2700		288	1	0.066			
1.0542	HTLWKACILY	10	HSV	adr	POL	723	1	0.030			
2.0231	TSCPPICECY	10	HBV	ads	1	226	1	0.018			
2.0246	KSVQHLESLY	10	HBV	adw .		1.161	1	0.016			
1.0910	NLYVSLLLLY	10	HSV	adr	POL	1059	1	0.015			
1.0901	WMMWYWGPSL	10	HBV	adr	ENV	359	2.1	0.0009	0.519	0	38
2.0089 I	LLYQTECRK	9	HBV	ayw	POL	1094	3		1.8	0.44	
20116	IMPARFYPK	9	HSV	2700		713	3		0.59	1.5	
2.0082	CLHQSPVRK	9 1	HBV	ayw	POL	147	3		0.14	0.025	
5.0056	SAICSVVRR	9 1	HBV	i	POL	531	3		€0.0003	0.047	
2007											
	HLHQOIIKK	9	HBV	1 ayw	POL	646	3		0.043	0.0075	
			HBV HBV	ayw	POL	1197					
2.0219	HLHQOIIKK	9					3		0.041	0.0075	
2.0219 2.0234 2.0235	HLHQDIIKK SLPQEHIIQK	9	HBV	ayw		1197	3		0.041	42	
2.0219 2.0234 2.0235	HUHQOTIKK SUPQEHIIQK SMIPSCCCTK	10	HBV	agw ads/adw	POL POL	1197 295 295 445	3 3 3 3		0.041 0.34 0.43 1.1 0.15	0.0075 4.2 1.9 1.79	
2.0219 2.0234 2.0235 5.0107 2.0214	HLHQOIIKK SLPGEHIIQK SMPPSCCCTK SMYPSCCCTK QAFTPSPTYK LLLYQTFCRK	9 10 10 10 10 10	HBV HBV HBV	adr/adw ayw	POL	1197 295 295 445 1083	3 3 3 3 3		0.041 0.36 0.43 1.1 0.15	0.0075 4.2 1.9 1.79 1.3 0.021	
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245	HLHQDIIKK SLPQEHIIQK SMPPSCCCTK SMYPSCCCTK QAFTESPTYK LLLYQTFGRK YMDDVVLGAK	9 10 10 10 10 10 10	HBV HBV HBV HBV	ayw adr/adw ayw	POL POL POL	1197 295 295 295 445 1083 1,123	3 3 3 3 3 3		0.041 0.36 0.43 1.1 0.15 0.89	0.0075 4.2 1.9 1.79 1.3 0.0271	
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245 5.0100	HLHQDIIKK SLPQEHIIQK SMPPSCCCTK SMYPSCCCTK QAFTPSPTYK LLLYQTFGRK YMDDVVLGAK TSAKSVVRR	9 10 10 10 10 10 10	H8V H8V H8V H8V H8V H8V	adr/adw ayw	POL POL POL	1197 295 295 445 1083 1,123 530	3 3 3 3 3 3 3		0.041 0.36 0.43 1.1 0.15 0.89 0.16	0.0075 4.2 1.9 1.79 1.3 0.028 0.0076	
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245 5.0108 2.0094	HLHQDIIKK SLPQEHIIQK SMPPSCCTK SMYPSCCTK QAFTPSPYYK LLLYQTFCRK YMDDVVLCAK TSAICSVVRR PTYKAFLOX	9 10 10 10 10 10 10 10	HBV HBV HBV HBV HBV HBV HBV	ayw adr/adw ayw ALL	POL POL POL POL POL	1197 295 295 645 1083 1,123 530 1263	3 3 3 3 3 3 3 3		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	
2.0219 2.0234 1.0235 5.0107 2.0214 2.0245 5.0108 2.0094 2.0068	HLHQDIIKK SLPQEHIIQK SMPPSCCTK SMYPSCCTK QAFTPSPTYK LLLYQTFCRK YMDDVVLGAK TSAKSVVRR PTYKAFLOK PTDLEAYFK	9 10 10 10 10 10 10 10 10 9	HBV HBV HBV HBV HBV HBV HBV HBV	ayw adz/adw ayw ayw ALL ayw adw	POL POL POL	1197 235 235 445 1083 1,123 530 1243 1,552	3 3 3 3 3 3 3 11		0.041 0.36 0.43 1.1 0.15 0.89 0.16	0.0075 4.2 1.9 1.79 1.3 0.028 0.0076	
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245 5.0108 2.0094 2.0068	HLHQDIIKK SLPQEHIIQK SMPPSCCTK SMPPSCCTK QAFTPSPTYK LLLYQTFCRK YMDDVVLGAK TSAKSTVVRR PTYKAFLCK PTDLEAYFK KYTSPPWLL	9 10 10 10 10 10 10 10 10 10 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adz/adw ayw ayw ALL ayw adw	POL POL POL POL POL	1197 235 235 445 1083 1,123 530 1263 1582 1,330	3 3 3 3 3 3 3 11 11 11		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245 5.0108 2.0094 2.0068 2.0061 2.0059	HLHQDIIKK SLPQEHIIQK SMPSCCCTK SMPSCCCTK QAFTESPTYK LLLYQTFCRK YMDDVVLCAK TSAKSIVVRR PTYKAFLOK PTDLEAYFK KYTSFPWLL LYAAVTNFL	9 10 10 10 10 10 10 10 10 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ayw ALL ayw adw ALL	POL POL POL POL POL	1197 235 235 645 1083 1.123 530 1263 1.562 1.330 1.169	3 3 3 3 3 3 3 3 11 11 11 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3
2.0219 2.0234 2.0235 5.0107 2.0214 2.0245 5.0708 2.0094 2.0068 2.0061 2.0059 2.0046 1	HLHQDIIKK SLPQEHIIQK SMPPSCCCTK SMYPSCCCTK SMYPSCCCTK QAFTESPTYK ULTYTFORK YMDDVVLCAK TSAKSSVVRR PTYKAFLCK PTDLEAYFK KYTSPPWLL LYAAVTNFL FYPNLTKYL	9 10 10 10 10 10 10 10 10 9 9 9 9 9 9 9	H8V H5V H5V H5V H5V H5V H5V H5V H5V H5V H5	ayw adr/adw ayw Ayw ALL ayw adw adw adw adw	POL POL POL POL POL	1197 235 235 445 1083 1.123 530 1243 1552 1.330 1.149	3 3 3 3 3 3 3 3 11 11 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3 2
2.0219 2.0234 1.0235 5.0107 2.0214 2.0245 5.0108 2.0094 2.0094 2.0099 2.0099 2.0099 2.0099 2.0046 2.0045 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK ULLYQTFCRK YMDDVVLCAK TSAKSVVRR PTYKAFLCK PTDLEAYFK KYTSFPWLL LYAAVTNFL FYPNLTKYL LYSSTVPSF	9 10 10 10 10 10 10 10 10 10 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw adw adw adw adw	POL POL POL POL POL	1197 235 235 445 1083 1.123 530 1243 1552 1.330 1.149 489	3 3 3 3 3 3 3 3 11 11 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	1. 2
2.0219 2.0234 2.0235 5.0107 2.0235 5.0107 2.0234 2.0235 2.0236 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK ULLYQTFCRK YMDDVVLCAK TSAICSVVRR PTYKAFLOK PTDLEAYFK KYTSPWLL LYAAVTNFL FYPNLTKYL LYSSTVPSF FYPKVTKYL	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw ALL adw adw adw adw adw	POL POL POL POL POL	1197 295 295 445 1083 1.123 530 1263 1552 1.330 1.169 489 465 718	3 3 3 3 3 3 3 3 3 11 11 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	1. 1.
2.0219 2.0234 1.0235 5.0107 2.0214 7.0215 5.0107 2.0214 7.0245 7.0	HLHQOIIKK SLPQEHIIQK SMPSCCTK SMYPSCCTK QAFTPSPYYK LLLYQTFCRK YMDDVVLCAK TSAICSVVRR PTYKAFLOX PTDLEAYFK KYTSPPWLL LYAAVINFL FYPNLTKYL LYSSTVPSF FYPKVTKYL FYPNVTKYL	9 10 10 10 10 10 10 10 10 10 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw ALL adw adw adw adw adw adw adw adw adw adw	POL POL POL POL POL	1197 285 295 645 1083 1.123 530 1263 1552 1.330 1.169 649 645 718	3 3 3 3 3 3 3 3 3 3 3 3 11 11 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	1. 1.
2.0219 2.0234 2.0235 5.0107 2.0214 2.0215 5.0107 2.0214 2.0245 2.0245 2.0266 2.0266 2.0266 2.0266 2.0266 2.0266 2.0266 2.0266 2.0266 2.0267 2.0268 2.0	HLHQDIKK SLPQEHIIQK SMPPSCCTK SMYPSCCTK QAFTPSPTYK LLLYQTFCRK YMDDVVLGAK TSAKSVVRR PTYKAFLCK PTDLEAYFK KYTSPPWLL LYAAVTNFL LYSSTVPSF PYPKVTKYL LYSSLSPFL	9 10 10 10 10 10 10 10 10 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw ALL adw adr adr adr adw ayw adw ayw ayw	FOL FOL FOL FOL TOL	1197 295 295 645 1083 1.123 530 1263 1552 1.330 1.149 645 718 718 368	3 3 3 3 3 3 3 3 3 3 11 11 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.0 3.1 1.1 1.0 0.5
2.0219 2.0234 1.0235 5.0235 5.0209 2.0245 2.0259 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMYPSCCCTK SMYPSCCCTK QAFTESPTYK LLLYQTFORK YMDDVVLCAK TSAKSVVRR PTYKAFLCK PTDLEAYFK KYTSPPWLL LYAAVTNFL FYPNLTKYL LYSSTVPSF FYPKVTKYL LYSISPFL LYSSTVPVL	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw Ali ayw Ali adw adw adr adw/ayw adw ayw adw ayw adw	POL POL POL POL POL	1197 295 295 446 1083 1,123 530 1263 1,330 1,149 449 466 718 718 366 6,36	3 3 3 3 3 3 3 3 3 3 3 11 11 11 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	1. 1. 1. 0.5
2.0219 2.0234 1.0235 5.0107 2.0245 5.0109 2.0246 2.0266 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK QLFTPSPTYK LLLYQTFGRK YMDDVVLGAK TSAKSVVRR PTYKAFLCK PTDLEAYFK KYTSPPWLL LYAAVTNFL FYFNLTKYL LYSSTVPSF FYPKVTKYL LYSISPFL LYSISPFL LYSISPFL LYSITVPVL LYSISPFL LYSITVPVL LYNILSPFL	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	H8V H8V H8V H8V H8V H8V H8V H8V H8V H8V	ayw adr/adw ayw ALL ayw adw adw adw adw adw adw adw adw adw ad	FOL FOL FOL FOL TOL	1197 285 295 445 1083 1.123 530 1.243 1.552 1.330 1.146 469 465 718 718 368 6.36 368	3 3 3 3 3 3 3 3 3 3 3 11 11 12 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	1. 1. 1. 0.9
2.0219 2.0234 1.0235 5.0107 2.0214 1.225 5.0109 2.0214 2.0245 2.0268 2.00	HLHQOIIKK SLPQEHIIQK SMPPSCCCTK SMPPSCCCTK QAFTPSPTYK QAFTPSPTYK LLLYQTFCRK YMDDVVLGAK TSAKSVVRR PTYKAFLOK PTDLEAYFK KYTSPWLL LYAAVTNFL FYFNLTKYL LYSSTVFSF FYPKVTKYL LYSILSPFL LYSSTVPVL LYSITPPVL LYSITPPVL LYSITPPVL LYNILSPFL LYSITPPVL LYNILSPFL LYNILSPFL LYNILSPFL LYNILSPFL LYNILSPFL	9 10 10 10 10 10 10 10 10 10 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw adw adw adw adw adw adw adw adw ad	FOL FOL FOL FOL TOL	1197 295 295 445 1083 1263 1263 1263 1263 1263 1263 1264 1265	3 3 3 3 3 3 3 3 3 3 3 3 11 11 11 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.1 2.1.1 11.1 0.5 0.5 0.5
2.0219 2.0234 7.0235 7.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK ULLYQTFCRK YMDDVVLCAK TSAKSVVRR PTYKAFLOK PTDLEAYFK KYTSPPWLL LYAAVTNFL FYFNLTKYL LYSSTVPSF FYPKVTKYL LYSSTVPSF LYSSTVPVL LYSTVPVL LYSTVPXL	9 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw ALL adw adw adw adw adw adw adw adw ayw adw ayw adw ayw adw ayw adw ayw	FOL FOL FOL FOL TOL	1197 295 295 445 1083 1.123 530 1243 1552 1.330 1.140 446 718 718 368 636 991 743	3 3 3 3 3 3 3 3 3 3 3 11 11 11 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.2 2.1.1.1.1.1.0.1 0.1.0.1.0.1.1.1.1.1.1.1.1
2.0219 2.0234 2.0234 2.0235 3.0107 2.0214 2.0214 2.0294 2.0058 2.0059 2.0059 2.0059 2.0045 2.0045 2.0045 2.0049 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0039 2.0035 2.0035 2.0035 2.0035 2.0037 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCTK SMYPSCCTK QAFTPSCCTK QAFTPSCCTK QAFTPSCCTK QAFTPSCCTK QAFTPSCCTK QAFTPSCCTK QAFTPSCCTK YMDDVVLCAK TSAICSVVRR PTYKAFLOK PTDLEATFK KYTSFPWLL LYAAVTNFL FYPNLTKYL LYSSTVPSF FYPKVTKYL LYSSTVPSF FYPKVTKYL LYSSTSPFL LYSSTVPVL LYSSTSPFL LYSSTVPVL LYSSTSPFL NYRVSWPKF HYPQTRHYL HYFKTRHYL	9 10 10 10 10 10 10 10 10 10 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw adw ALL adw adr adw adr adw ayw adw ayw adw ayw adr adr adr adr	FOL FOL FOL FOL TOL	1197 295 295 646 1083 1.123 1.263 1.263 1.263 1.263 1.263 1.263 1.264	3 3 3 3 3 3 3 3 3 3 3 3 3 11 11 11 24 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.1 2.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1
2.0219 2.0234 2.0234 2.0235 3.0107 2.0214 2.0236 2.0094 2.0058 2.0058 2.0058 2.0049 2.0039 2.0039 2.0038 2.0038 2.0038 2.0038 2.0038 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0036 2.0037 2.0036 2.0036 2.0037 2.0036 2.0037 2.0036 2.0037 2.0036 2.0036 2.0037 2.0036 2.0036 2.0037 2.0036 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMPSCCCTK SMYPSCCCTK QAFTESPTYK LLLYQTFCRK YMDDVVLCAK TSAKSTVRR PTYKAFLCK PTYKAFLCK PTOLEAFOR KYTSPPWLL LYAAVINFL FYFNLTKYL LYSSTVPSF FYPKVTKYL FYPNVTKYL LYSILSPFL LYSSTVPVL LYSILSPFL LYSSTVPVL LYNILSPFL NYRVSWPKF HYPQTRIHYL GYPALMPLY	9 10 10 10 10 10 10 10 10 9 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw Ali ayw Ali adw adw adw adw adw ayw adw ayw adw ayw adw Ali ayw adw Ali Ali Ali Ali Ali Ali Ali Al	FOL FOL FOL FOL FOL FOL TO	1197 295 295 646 1083 1.123 1.230 1263 1.263 1.330 1.169 646 718 718 368 636 366 991 743 714 1.224	3 3 3 3 3 3 3 3 3 3 3 3 11 11 24 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.1 2.1.1 11 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3
20219 2.0234 2.0235 5.0109 2.0245 5.0109 2.0246 2.02	HLHQOIIKK SLPQEHIIQK SMPPSCCTK CLLYQTFCRK TSACSVVRR PTYKAFLCK PTDLEAYFK KYTSPWLL LYSAVTNFL FYPNLTKYL LYSSTVPSF FYPKVTKYL FYPNVTKYL LYSISPFL LYSSTVPVL LYNILSPFL NYRVSWPKF HYPQTRHYL HYPKTRHYL CYPALMPLY AYRPPNAPI	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	H8V H8V H8V H8V H8V H8V H8V H8V H8V H8V	ayw adr/adw ayw All ayw All adw adw adw adr adw ayw adw ayw adw All All All All All All All A	FOL FOL FOL FOL NUCXNUCFU	1197 295 295 646 1083 1.123 530 1263 1.552 1.330 646 646 718 646	3 3 3 3 3 3 3 3 3 3 3 3 3 11 11 124 24 24 24 24 24 24 24 24 24 24 24 24 2		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3.1 2.1.1 11 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0
2.0219 2.0234 1.0235 5.0107 2.0235 5.0107 2.0245 7.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMPSCCCTK SMYPSCCCTK QAFTSPTYK QAFTSPTYK QAFTSPTYK YMDOVVLGAK TSAKSVVRR PTYKAFLCK PTDLEAYFK KYTSPWLL LYAAVTNFL FYFNLTKYL LYSSTVPSF FYPKVTKYL LYSISPFL LYSSTVPVL LYSISPFL LYSISPFL NYRVSWPKF HYRQTRHYL HYFKTRHYL GYPALMPLY AYRPPNAPI LYQTFGRKL	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	H8V H8V H8V H8V H8V H8V H8V H8V H8V H8V	ayw adr/adw ayw All ayw All adw adw adw adr adw ayw adw ayw adw All All All All All All All A	FOL FOL FOL FOL FOL FOL TO	1197 295 295 645 1083 1.123 530 1263 1.330 1.433 1.330 1.430 665 718 665 718 636 645 743 743 743 743 743 1.224 1.31 1.085	3 3 3 3 3 3 3 3 3 3 3 3 3 3 11 11 12 4 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3. 2. 1. 1. 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.
2.0219 2.0234 1.0235 5.0107 2.0245 5.0108 2.0246 2.0245 2.0246 2.0058 2.0058 2.0058 2.0058 2.0058 2.0059 2.0038 2.0051 2.0038 2.0051 2.0038 2.0051 2.0059 2.0038 2.0051 2.0055 2.0055 2.0055 2.0055 2.0055 2.0055 2.0055 2.0055 2.0056 2.0055 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK QAFTPSPTYK LLLYQTFGRK YMDDVVLGAK TSAKSVVRR PTYKAFLCK PTDLESYFK KYTSAPWLL LYAAVTNFL FYFNLTKYL LYSSTVPSF FYPKVTKYL LYSSTVPVL LYSILSPFL LYSSTVPVL LYNILSPFL NYRVSWPKF HYPGTRHYL HYPKTRHYL GYPALMPLY AYRPPNAPI LYQTFGRKL SYQHFRRLL	9 10 10 10 10 10 10 10 10 10 9 9 9 9 9 9	HSV HSV HSV HSV HSV HSV HSV HSV HSV HSV	ayw adr/adw ayw ALL ayw adw ALL adw adr adw/ayw adw adw adr adr adr ALL adr ALL adw adr ALL adw adr ALL adw adr adw adw adr adr adr adr adr adr adr adr adr adr	FOL FOL FOL FOL NUCXNUCFU	1197 295 295 445 1083 1263 1263 1263 1263 1263 1263 1263 1263 1264 1265	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 24 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3. 2. 1. 1. 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
2.0219 2.0234 1.0235 5.0107 2.0245 5.0109 2.0246 2.0266 2.0	HLHQOIIKK SLPQEHIIQK SMPSCCCTK SMPSCCCTK SMYPSCCCTK QAFTPSPTYK QAFTPSPTYK LLLYQTFCRK YMDDVVLCAK TSAKSVVRR PTYKAFLOK PTDLEAYFK KYTSPWLL LYAAVTNE FYPNLTKYL LYSSTVPSF FYPKVTKYL LYSSTVPSF FYPKVTKYL LYSSTVPVL LYSTVPNVTKYL LYSSTVPVL LYSTVPNVTKYL HYFKTRHYL CYPALMPLY AYRPPNAPI LYQTFCRKL SYQHFRRLL LYSHPIILGF	9 10 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	H5V H5V H5V H5V H5V H5V H5V H5V H5V H5V	ayw adr/adw ayw ALL ayw ALL adw adw adw adw adw ayw adw ayw adw ayw adw ALL adw ALL adw ALL adw ALL adw ALL adw ALL adw ALL adw ALL adw ALL adw Ayw Ayw Ayw Adr ALL Ayw Adr ALL Ayw	FOL FOL FOL FOL NUCXNUCFU	1197 295 295 645 1083 1.123 530 1263 1.330 1.433 1.330 1.430 665 718 665 718 636 645 743 743 743 743 743 1.224 1.31 1.085	3 3 3 3 3 3 3 3 3 3 3 3 3 3 11 11 12 4 24 24 24 24 24 24 24 24 24 24 24 24		0.061 0.36 0.43 1.1 0.15 0.99 0.16 0.0006	0.0075 4.2 1.9 1.79 1.3 0.021 0.0076 0.713	3. 2. 1. 1. 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.

Table 23(d)





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Peptide	Sequence	, 44	Virus	Strain	Molecule	Pos.	iotif	A1	A3.2	A11	A24
2.0174	SYCHPURLL	10 i	HBV	avw		407	24				0.16
2.0173	SYCHERKLLL	10 I	HBV	adr/adw	1	578	24				0.066
2.0176	YYFEHLVNHY	10	Hav	ayw	1	735	24				0.040
2.0172	AYRI PNAPIL	101	HBV	ALL	<u> </u>	521	24				0.022
2.0171	CYRWMCLERF	101	11.0 -	ALL		234	24				0.011
5.0115	NFLISLCIAL	10	HBV	- 1	POL	1090	3,11		0.31	7.4	0.0099
1.0307	YVSLMLLYK	9	HBV	adr	POL	1066	3,11		50	0.30	
1.0379	LLYKTYCKK	9	HRV	adw	POL	1095	3,11		25	0.40	
1,0370	VINCYLPLOK	9	HBV	-dw	POL	722	3,11		0.014	1.3	
1.0176	RHYLHTLWK	1 9	HBV	adr	POL	719	3.11		1.2	0.010	
1.0367	STYPSPNPK	9	HBV	adw	POL	668	3,11		0.021	0.93	
1.0215	TTOLEAYFK	9	HBV	adr	<u>x</u>	1523	3,11		0.0004	0.92	
1.0848	YVSLLLYK	191	HBV	adr	POL	1274	3,11		0.39	0.92	
1.0363	PTYKAFLTK HLYPVARQR	9	HBV	adw adr	POL	1257	3,11		0.54	0.0020	
1.0356	STNRQLCRK	9	HBV	adw	ENV	55	3,11		0.51	0.34	
1.0991	ALRFTSARR	9 1	HBV	adr	*	1488	3.11		0.44	<0.0005	
1.0197	PVNRPIDWK	9	HBV	adr	POL	1197	3,11		0.000	0.41	
1.0360	TVNENRELK	•	HEV	-dw	POL	703	3.11		0.016	0.40	
1.1041	VVNHYPQTR	•	HBV	adw .	POL	740	3,11		0.030	0.33	
1.0152	SITSTCPCK	•	HBV	adr	ENV	1505	3,11		0.011 0.10	0.28	
1.0213	CANTHETHIK	9	HBV	adr	POL	643	3.11		0.003	0.23	
1.0374	CLHQSAVRK	+ 7 +	HBV	adw	POL	578	3.11		0.22	0.017	
1,0980	VVDPSQFSR	1 9	HBV	adr	POL	963	3,11		0.011	0.20	
1.0362	PLYACIQAK			adw _	POL.	1259	3,11		0.18	0.034	
2.0074	YVNTNMCLK	,	HBV	ayw	CORE	507	3,11		0.16	0.048	
1.0177 1	PLYACIQSK	9 1		adr	POL	1230	3,11		0.11	0.018	
1.0972	RLADEGLNR	9	HBV	adr	POL	601	3,11		0.10	0.025	
1.0976	AVNHYPKTR	9	HBV	eds	POL	711 680	3,11		0.0071	0.096	
1.0975	RLKLMPAR	9		adr adr	POL	730	3.11		0.095	<0.0005	
1.0977	ILYKRETTR KVFVLCCCR	9	HBV	ed?	3	1548	3,11		0.012	0.082	-
1,0165	NVSIPWIHK	9	HBV	adr	POL	622	3,11		0.072	0.076	
1,0962	LLLYKTRCK	9	HBY	adr	POL	1065	3,11		0.072	0.0045	
1.0978	RLVPQTSTR	9	HSV	adr	POL	757	3,11		0.048	0.0032	
1.0219	FYLCCCILHX	9	HBV	adr	ズ	1550	3,11		0.065	0.019	
1.1042	RLVLQTSTR	9	HBV	adw	POL	786	3,11		0.064	0.0002	
1.1043	MLLYKTYCK	9	HBV	-dw	POL	1094	3,11		0.061	0.00312	
1.0170	TVNEKRRLK	9	HBV	adr	POL	1296	3,11		0.042	0.0071	
1.1045	NLYPVARQR LPYRPTICE	9	HBV	adw .	POL	1407	3.11		0.021	0	
1.0845	LVSPCVWIR	9	HBV	adr	CORE	509	3.11		0.0033	0.020	
1,0961	LVCSSCLPR	9 1	HBV	adr	POL	1022	3.11		0.0008	0.015	
1.0967	HISOLTFOR	•	HBV	adr	CORE	494	3.11		0.013	0.011	
1.1047	SVPSRLFOR	•	HSV	adw	POL	1424	3.11		0.0007	0.010	
1.0909	SVPSHLPDR	9	HBV	i adr	POL	1395	3,11		0.0004	0.010	
1.0564	TLPQEHIVLK	10	HBV	i adr	POL	1179	3.11		0.092	5.6	
2.0205	TVPVFNPHWK	10 1		i ayw	POL	724	3.11		3.5	1.0	
1,0643	TLWKACILYK SMYFSCCCTK	10	HBV	adr	ENV	295	3,11		15	3.4	
1.1153	RUPYRPTICK	10	HBV	ayw Mw	POL	1406	3,11		2.8	0.030	-
1.0584	STTDLEAYPK	10	HBV	adr	×	1522	3,11		0.0066	2.7	
1.0554	LLLYKTPCKK	10	HBV	adr	POL	1045	3.11		2.5	0.012	
1.0799	TVNAHRNLPK	10	HBV	adw_	x	1529	3,11		0.82	0.65	
1.0584	EAYFKDOLFK	10	HBV	adr	x	1527	3,11		0.037	0.74	
1.1051		10	HBV	eds	POL	962	3.11		0.0009	0.63	
1.0789		10	HBV	adw	POL	1094 858		 	0.61	0.020	
1.0546		10	HBV	edr edr	POL	1150		 	0.20	0.092	
1.1152	RLGLYRFLLR	10	HBV	adw adw	POL	1397		 	0.19	0.0069	
1.0547		10		ad?	POL	943	3,11	1	0.035	0.17	1
1.1150		10		adw .	POL.	962	3.11		0.17	0.0003	
1.0541		10	HSV	adr	x	1500	3,11		0.073	0.092	Γ
1.1091		10	HBV	adr	POL	1377			0.077	0.043	
1.1072		10	HBV	ad r	CORE	532			<0.0003	0.075	<u> </u>
1.1089		10	HBV	9d1	POL	1320		 	0.025	0.072	
1.1071		10	HBV	adr	CORE	531			0.0005	0.068	
2.0210		10	HBV	i ayw	POL POL	721	3.11	 	0.007	0.053	
1.1146		1 10		. dw	POL	923	3.11	 	0.029	0.0087	
				+	POL	721		 	<0.0004	0.023	+
1.0781	NVTKYLPLOK	10	· UBA	<u>adw</u>	·		. 3,41	<u> </u>	1		1

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	6		Virus	Strain	Molecule	Pa	. Motif	A1	A32	A11	A24
Peptide	Sequence				X	1422	3.11		0.0019	0.023	
1.1092	RVCCQLDTAR	10	HBV	ed t							
1.0793	SLGIHLNPOK	1 10 1	HSV	ad w	POL	1177	3,11		0.017	0.014	L
1.0909	YLYSPCYWIR	10	HSV	edt	CORE	508	3.11		0.015	0.0027	
2.0207	FYCFLTYNEK	10	Hav	270	POL	698	3.11		0.0057	0.015	
				ed?	POL	440	3.11	-	0.0040	0.014	
1.0535	YVCPLTVNEX	10	H5V	807							
1.1075	RLADECLNRR	10	HBV	adr	POL	401	3,11		0.013	0.0004	
1.1086	TYLKLKOCTK	10	HeV	841	POL	1185	3,11		0.013	0.0024	
					ENV	314	3.11		<0.0003	0.010	
1.0773	PIPSSWAFAK	10	HBY	1 20 -							
1.0778	LTVNENRRLK	10	HEV	adw	POL	702	3.11		0.0025	0.00795	

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	dotif	A1	A3.2	All	A24
1.0118 1	CTCCSSDLY	i 9 i	HCV		LORF	1123	1	3.0	0	0.010	
1.0112	NIVOVOYLY	1 9 1	HCV	,	NST/ENV2	697	1	0.40	0	0.010	
2.0034	VQDCNCSIY	9 1	HCV			302	1	0.54	0.0005	0.0003	-
2.0035	LTPROMVDY	9	HCY	:		605	1	0.078			
1.0145	RVCEKMALY	9 1	HCV	t	LORF	2588	1	0.053			
1.0140	DVVCCSMSY	9	HCV	1	LORF	2416	1	0.039		·	
2.0036	PTIFKIRMY	9	HCV			436	1	0.012			
1.0509	CLSAPSLHSY	10	HCV	!	LORF	2888	1	0.41	0.013	0.0034	0.0002
1.0499	TLHCPTPLLY	10	HCV	1	LORF	1617	1	0.30	0.11	0.0024	
2.0037	EYVLLEL	7	HCV		1	719	24				1.4
2.0169	MYVOCVEHIRL	10	HCV			633	24				0.026
2.0170	EYVULFUL	10	HCV			719	×				0010
1.0139	SVPABILEK	9	HCV		LORF	2269	3.11		0.016	0.07	
1.0955	QUFTPSPER	9	HCV		ENVI	290	3,11		0.75	0.033	
1.0090	RLCVRATRK	9	HCV		CORE	43	3,11		0.74	0.16	
1.0123	LIPCHSKKK	9	HCV		LORF	1391	3,11		0.54	0.19	
1.0122	HLIPCHSKIK	9	HCV		LORF	1390	3.11		0.25	0.010	
1.0952	KTSERSOPR	9	HCV		CORE	51	3,11		0.16	0.054	
1.0120	AVCTRGVAK	9	HCV		LORF	1183	3,11		0.016	0.038	
1.0143	EVICVOPEK	191	HCV		LORF	2543	3,11		0.0019	0.093	
1.0137	MIKVESENK	9	HCV		LORF	2261	3,11		0.015	0.0079	
1.0957	CITISLICK	9	HCV		LORD	1042	3,11		0.0095	0.011	
1.0496	CVACALVAFK	10	HCV	_	LORD	1858	3,11		0.87	1.1	
1.0480 i	HLHAPTC9CK	10	HCV		LORF	1227	3,11		0.57	0.0051	
1.1062	RMYYCCVEHIR	10	HCV		NS1/ENV2	632	3,11		0.27	0.012	
1.0485	HLIPCHSKKK	10	HCV		LORF	1390	3,11		0.27	0.025	
1.0484	TLCPCAYMSK	10	HCV		LORF	1251	3,11		0.17	0.13	
1.1067	CVCIYLLPNR	10	HCV		LORF	3002	3.11		0.0029	0.032	
1.1063	LLFLLLADAR	10 i	HCV		NSI/ENV2	723	3,11		0.015	0	

Table 23(e)





.					1		ı				
Peptide	Sequence	1 44	Virus	Strain	Molecule	Pos.	dotif	A1	A32	A11	A24
1,0014	FRDYVDRFY	9 1	HIV	 	CAG	798	1	0.090			
2.0129	MOYMDOLY	191	HOV	·	1	875	1	0.064			
1.0028	TVLDVCDAY	,	HIV		POL	802	1	0.018			
1.0412	YTYLDYCDAY	10	ни	1	POL	801	1	0.28	0	0.0004	
1.0415	VIYOYMDOLY	10	HIV	<u> </u>	POL	874	1	0.25	0.0007	0.0090	
2.0252	VTVLDVCDAY	10	HIV	 		801	1	0.000			
1,0431	EVNIVIDEOY	10	HIV	1	POL	1187	1	0.053			
1.0441	LVAVHVASCY	10	нν		POL	1329	1	0.039			
1.0442	PAETCOETAY	10	НΙΥ	į.	POL	1345	1	0.013			
2.0251	ISKICPENPY	10	HIV	Ť		742	1	2013			
2.0255	QMAVFIHNFK	10	VIH.	1		1,432	3		0.61	0.64	
2.0064	RYLKDOOLL	19	HIV	†		2,778	24				076
2.0134	KYLKDOOLL	9 1	НΙΥ	† · · · · · · · · · · · · · · · · · · ·		2,778	24				0.32
2.0065	TYONOEPF	9	HIV	1		1,033	24				0.30
2.0131	TYONGER	9	HIV	1	1	1,033	24				0.20
2.0063	IYOEPFIONL	9	ни	1	1	1,036	24				0.052
2.0132	MOEPFIONE	9	HIV		T	1,036	ж				0.033
2.0066	NOMEDOLY	,	HIV			\$75	24				0.013
2.0247	PYKRWIILCL	10	HIV		1	266	24				0.017
2.0190	MORWILLOL	10	HIV			266	24				0.014
2.000	LYPLASLISL	10	HIV			506	×				0.014
1.0050	KLACEWFYK	,	HIV	I	POL	1,358	3,11		ט	0.000	
1.0944	AVPIHINFKE	9	HIV		POL	1434	3.11		0.17	1.8	
1.0082	ALFQ95MTK	•	HIV		POL	123	3,11		1.1	0.96	
1.0046	IVIWCKTPK	9	НΙΥ		POL	1075	3.11		0.085	0.37	
1.0079	KLTEDRWNK	9	HIV		VIF	1712	3,11		0.013	0.27	
1.0027	CIPHPACLK	•	HIV		POL.	788	3.11		0.23	0.065	
1.0059	QHBQLIKK	1 9 1	нον		POL.	1215	3.11		0.0091	0.16	
1.0939	KIWFSYKCR	9 1	HIV	1	GAG	443	3.11		0.12	0.0005	
1.0072	DATDIQTK	191	HIV	1	POL,	1458	3.11		0.025	0.098	
1.0036	MCYELHPOK	9	HOV	!	POL	925	3.11		0.064	0.096	
1.0062	YLAWVPAHK	9	HIV		POL	1227	3,11		0.077	0.057	
1.0936	KIWFSHKCR	9	HIV	1	CAG	443	3,11		0.027	<0.0005	
1.0047	FYNTPPLYK	•	HOV		POL	1111	3,11		0.012	0.044	
1.0024	NTPVFAIKK	•	HIV	1	POL	752	3.11		0.033	0.060	
1.0080	TVQCTHCIK	,	HIV		D/V	2420	3,11		0.0021	0.046	
1.0013	ILDINGCPK	,	HIV		CAG	257	3.11		0.012	0.0004	
1.0015	RDYVDRFYK	,	HIV		GAG	259	3.11		0.0007	0.040	
1.0058	GIIQAQPDK	9	HIV		POL	1199	3,11		<0.0009	0.040	
1.0064	VLPLDCIDK	9	HIV		POL	1254	3,11		0.038	0.032	
1.0026	LVDFRELNK	•	HIV		POL	740	3.11		0.011	0.030	
1.0078	KVVPRRKAK	9	НΙΥ		POL	1513	3.11		0.029	0.0039	<u> </u>
1.0942	MTKILEFFR	7 9	HIV		POL	. 259	3.11		<0.0008	0.016	
1.0463	TVYYCVPVWK	10	HIV	1	ENA	2125	3.11		3.8	7.3	
1.0418	TVQPTVLPEK	10	HIV		POL	935	3.11		0.16	5.6	<u> </u>
1.0447	AVFIHNFKRK	10	HIV	i	POL	1434	3.11		0.66	0.85	
1.007	KYLFLDCIDK	10	HIV	<u> </u>	POL	1253	3.11		0.36	0.78	
1.0408	KLVOFRELNK	10	HIV	1	POL	748	3.11		0.51	0.090	<u> </u>
1.0403	KLICFGMDGPK	10	нач		POL	706	1.11		0.39	0.076	
1.0395	FLCKIWPSYK	10	HIV	1	CAC	440			0.32	0.024	
1.1056	KIQNFRYYYR	10	HIV	1	POL	104			0.032	0.21	
1.0410	CIPHPACLKK	10	HIV		POL	788	3.11		0.011	0.17	
1.00%	LVKLWYQLEK	10	HIV		POL.	1117		!	0.054	0.082	
1.0396	MICCICCFIK	10	HIV		POL	642	3,11		0.0099	0.055	
1.0413	MTKILEPFRK	10	HEV		POL	859	1.11		oors	0.038	
1.0453	VVIQONSDIK	10	HOV		POL	1504	3.11		<0.0005	0.021	ļ
1.0394	FLCKIWPSHK	10	HIV	1	CAG	440	3.11		0.020	0.00713	
1.1059	IVQQQNNLLLR	10	HIV	<u> </u>	EVA	2741	3.11	L	0.00224	0.019	
1.0417	FTTPDKKHQK	: 10	HIV	!	POL	909	3.11		<0.0003		
1.0405	LVEICTEMEK	10	HIV		POL	729	3.11		0.0002	0.012	
1.0372	LVQNANPDCK	10	HIV		CAG	327	3.11	L	<0.0002	0.011	

Table 23(f)

1 1			•			Ì				1	
Peptide	Sequence	1	Virus	Strain	Molecule	10-	Motif	A1	112	A11	A24
1.0225	SEYRHYCY	9 1	HPY	16	E4	80	1	7.5	0.0011	0.034	
1.0230	CAEPDRAHY	9 1	HPV	16	E7	44	1	0.021			
1.0610	LOCIETCYY	10 i	HPV	18	54	25	1	0.25	0.0054	0.012	
2.0159 i	YSKISEYRHY	10 i	HPV	16	E4	77	1	0.17	<0.0000	0	
20162	YSKISEYRHY	10	HPV	16	EA	77	-1	0.11	<0.000	0	
1.0599	HCDTPTLHEY	10	HPV	16	E7	2	1	0.087			
1.0601	OPETTDLYCY	10	HPV	16	E7	16	1	0.033			
1.0913	IHDULECVY	· 10 i	HPV	16	E4	30	1	0.033			
2.0160	YSRIRELRHY	. 10 1	HPV	18	E4	72	1	0.018			
2.0164	YSRIRELRHY	: 10	HFV	18	E4	72	1	0.012			
1.0594	AVCOKCLIOTY	· 10	HOPV	16	E4	4	1	0.0095			
2.0161	LLIRCLROOK	10	HPV	18	E4	101	3		0.081	0.078	
2.0032	HTMLCMCCK	1 9 1	HPV	18	Ð	59	11		0.020	0.079	
2.0029	VYOCTVLEL	; 9]	HIPV	18	E4	33	24				0.33
2.0027	CYSLYCTTL	1 9	HIPV	16	E4	Ø	24				0.057
2.0024	VYDFAFROL	9	HPV	16	£4	49	24				0.032
2.0031	LYNLLIRG	9	HIPV	18	E4	*	24				0.019
2.0030	VYCOTLEX.	1 9	HPV	18	E4	85	24				0.010
1.0239	SVYCDTLEK	9	HOPV	18	54	84	3.11		0.39	23	
1.0043	SVYCDTLEK	9	HPV	18	E6	84	3.11		0.55	1.1	
1.0244	SYYCOTLEK		HPV	18	56	84	3.11		ಬಾ	0.95	
1.0226	TTLEQQYNK	9	HPV	16	E4	73	3,11		0.010	0.67	
1.0241	SIPHAACHK	9	HPV	18	£4	59	3.11		0.00004	0.25	
1.0237	SIPHAACHK	•	HJPV	18	E4	59	3,11		0.017	0.12	
1.0233	IVOPICSQK	,	HIPV	16	Ð		3.11		0.035	0.023	
1.0997	KLAHLNEKA	9	HPV	18	EA	117	3.11		0.025	<0.0005	
1.0234	LIRCURCOK	. 9	HPV	18	E4	102	3.11		0.019	0.0013	
1.0853	IILECYYOK	. 9 1	HPV	16	E4	23	3.11		0.0076	0.019	
1.0999	CIDIFYSIUR	191	HPV	18	E4	68	3.11		0.017	COULS	
1.0998 1	CIDFYSRIE	9 1	HPV	18	EÁ	4	3.11		0.010	0.0009	
1.05%	CTTLEQQYNK	10	HPY	16	EA	92	3,11		0.010	0.98	
1.0606	LLURCLECOK	10	HPV	18	E4	101	3.11		0.076	0.29	
1.0598	LLIRCENCOK	10	HPV	16	EA	106	3,11		0.12	0.24	
1.0629	TTIKCTIKCOK	· 10	HIPV	18	E4	101	3,11		0.16	0.11	
1.0614	LTEVFEFAFK	10	HPV	18	E4	41	3.11		0.0000	0.11	
1.0605	CIVOPICSQK	10	HIPV	16	E7	-	3.11		0.0017	0.060	
1.0625	LTEVFEFARK	10	HPV	18	E4	41	3.11		0.0012	0.041	
1.0591	DULECVYCK	10	HIPV	16	E4	32	3,11		0.0065	0.021	
1.1101	KLRHLNEKKR	10	HUPV	18	E4	117	3.11		0.013	0	
1.1095	CVYCKQQLLIK	10	HPV	16	E4	37	3.11		0.011	0.0059	

Table 23(9)

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						1			1	}	1
Peptide	Sequence	144	Virus	Strain	Molecule	Pos.	Hotel	A1	A32	A11	A24
2.0020	EVDPICHLY	. 9	MAGE	3		161	1	18	0.0003	0.0009	
3.0172 i	EADPISATY	,	MACE	5/51		16	l l	9.9	0.000%	0.0006	0
1.0258	TODLYQEKY	. ,	MAGE	1		240	1	2.1	0	0.0003	
3.0173 1	EVDPICHVY	. 9	MAGE	6		161	1	1.9	<0.0003	<0.0003	0
1.0254	EADPTCHSY	•	MAGE	1		161	1	1.1	0	0	
1.0259	LVQEXYLEY	9	MAGE	1		243	_	0.42	0.0013	0.053	
6.0053	TSYVKVLEY	,	MAGE	1	New	275	1	0.099			
2.0009	SELPTTMINY	7	MACE	3	1	,	1	0.055			
2.0011	CSVVCNWQY	19	MAGE	3	1	77	1	0.050			
2.0008 I	SSPSTTENY	9	MAGE	2	1	•	1	0.043			
1.0252	MLESVIKNY	9	MAGE	1		128	1	0.011			
2.0147	ASSUPTIMENT	10	MAGE	3	†		1	2.6	<0.000€	0.033	
2.0167	LTQDLVQEKY	10	MAGE	1	1	239	1	1.2	<0.000	0.0073	
6.0114	EISYVKVLEY	10	MAGE	1	NEW	274	1	0.56	1		
2.0141	ASSISTIONY	10	MAGE	2	†	8		0.17	<0.000	0.026	
1.0648	DLYQEKYLEY	10	MAGE	1	 	242	1	0.044			
6.0065	TSYVKVLEY	9	MAGE	1	new	275	3		0.71	0.010	
4.0119	TTINFTROR	9	MACE	1		46	3		0.043	0.37	
6.0064	ALAETSYVK	9	MAGE	1	new	271	3		0.31	0.36	
4.0132	LTOOLVOEK	,	MACE	1		239	3		<0.0003	0.14	
6.0062	LVQEKYLEY	191	MAGE	1	New	243	3		0.000	0.034	
4.0131	HSAYCEPEK	9	MACE	1		229	3		0.014	0.000	
4.0122	LFRAVITKK	9	MACE	1		97	3		0.011	0.0005	
6.0124	RVRFFFFSLR	10	MAGE	1	new	290	3		0.43	0.000	
4.0161	ADLVCFLLLK	10	MAGE	1	† · · · · · · · · · · · · · · · · · · ·	107	3		0.35	0.29	
4.0160	ESLFRAVITK	10	MAGE	1		25	3.		0.14	0.088	
6.0119	DLYQEXYLEY	10	MAGE	1	new	242	3		0.032	0.0051	
6.0123	YVIKVSARVR	10	MAGE	1	New	283	3		0.019	0.0009	
4.0168	LSVMEVYDCK	10	MACE	1	1	218	3		<0.0008	0.012	
4.0163	KAEMLESVIK	10	MAGE	1	1	125	3		<0.0003	0.0097	
6.0125	RALAETSYVK	10	MACE	1	new	270	11		0.18	0.24	
2.0010 i	NYFLWSOSY	9	MAGE	3		16	24		1		0.027
2.0165	NYKHOFFEIF	10	MAGE	1	1	1.35	24		†		0.25
2.0151	LYMATCLCL	10	MAGE	3		115	24				. 0048
6.0126	SYVIKVLEYVI	10	MAGE	1	New	276	24		Ī		0.036
1.0248	SLFRAVITK	9	MAGE	1	1	- 15	3,11		4.1	27	
1.1006	SYMEVYDOR	1 9	MAGE	1	 	219	3.11		0.0083	13	
1.1004	TUNFTROR	9	MAGE	1	1	46	3,11		0.016	1.0	
1.0257	LTOOLVOEK		MAGE	i	†	239	3,11		0.0002	0.38	
1.0634	SLFRAVITKK	10	MAGE	1	†	1 %	3.11		1.2	0.96	
1.0647	LLTOOLVOEK	10	MAGE	i		238	3,11		0.0004	0.16	
1.0640	MLESVIKNYK	10	MAGE	1	T	128	3.11		0.14	0.027	
1.0644	LLGDNOMPK	10	MAGE	1/3	 	182	3.11		0.020	0.011	
1.0630	SLEORSLHCK	10	MAGE	1	 	1 2	3.11		0.015	0.015	

Table 23(h)

Peptide	Sequence		Virus	 Strain	Molecuie	P	Motti	A1_	A3.2	A11	A24
1,0281 1	CSDCTTIHY	9 1	p\$3	i	1	72%		29.5	0.0010	0.029	
1.0667	CTAKSVICTY	10	ρSJ	i		117	1	0.33	0.023	0.049	0
1.0672	RVECNILRVEY	10	p\$3	 		196	1 1	0.022			
1.02/8	RYRAMANK	9	653			156	3.11		1.5	0.73	
1.0276	CTYSPALNK	9	553			124	3,11		0.46	1.1	
			P53		 	311	3,11		0.000	0.095	
1.0285	NT966PQPK				 	283	3.11		0.0015	0.091	
1.0284	RTEEENLAK		p53		 	363	3.11		0.020	0.0052	
1.0287	ELNEALELK	9	<u>p\$3</u>	-	+	283	3.11		33	0.0000	
1.0678	RTEEENLRKK	10	p53	<u> </u>		101	3.11		2.5	0.88	
1.1113	KTYQCSYCFR	10	p53		ļ						
1.1115	VVRRCPHHER	10	p53		<u> </u>	172	3,11		0.099	0.0017	
1.0679	NTSSEPQPKK	10	لكم		<u> </u>	311	3.11		0.0005	0.054	
1.1121	RVCACPGRDR	10	p53		Ĭ	273	3,11		0.014	0.011	
1.1116	CLAPPOHLIR	10	p53			187	3,11		0.013	0.0006	

Table 23(i)

		TT		, , , /		/					i
Peptide	Sequence	1	Virus	Strain	Molecule	Pos	. Motif	A1	A3.2	A11	A24
3.0175 1	KCEYPVEMY	9 1	PAP	1		322	1	14	<0.0002	0.0000	0
3.0174	LCEYINGRY	191	PAP	1		81	1	0.78	<0.000	0.0003	0
3.0166	ASCHLTELY	91	PAP	i		311	1	0.77	<00000X	0.055	0
3.0163	ESYNCHECTY	91	PAP			95	1	0.096	<0.0003	0.0002	0
3.0237	RETETETA	10	PAP			238	1	Н	0.0036	0.0004	0
3.0235	(SELELELY	10	PAP			Z36		12	0.0005	0.0004	0
3.0736	LTOLCMEOHY	10 1	PAP			70	1	0.62	0.015	0.0024	0.0022
3.0238	KCEYFVEMYY	10 1	PAP	1		322	1	0.018			
3.0230	LVNEILNHMK	10	PAP			263	3		0.056	0.12	
3.0158	ATQUESYKK	191	PAP			274	11		0.10	1.2	
3.0231	ETUKSEEPOK	10 1	PAP			170	11		<0.0004	0.014	
3.0161	LYFEKCEYF	191	PAP			318	24				2.5
3.0160	LYCESVHNF	1 9 1	PAP			213	24				0.44
3.0159	PYXDRATL	191	PAP			183	24				0.11
3.0142	VYNCLLPPY	9	PAP			302	24				0.003
3.0232	PYASCHLTEL	10	PAP			309	24				0.024

Table 23(j)

Peptide	Sequence		4, Virus	& " Strain	Molecuie	/	. 10-45				
1.0270	ALPERITSLY	9 1		30218	Moterate		Mode	Al	A3.2	A11	1 124
2.0157	VSHSFPHPLY		PSA		 	231	1 1	0.011			
		10	ITSA :		<u> </u>	46	1	0.15	<0.0003	0.0015	
1.0265	PLYDMSLLK	' 9	P5A		<u> </u>	15	3,11		0.24	0.037	
1.0273	VVHYRKWIK	9	PSA			242	3.11		0.0072	0.093	
1.0272	YTKVVHYRK	7	PSA I			239	3.11		0.0006	0.058	
1.1009	SLUKNRFLR	9	PSA			100	3.11		0.0024	0.047	
1.0260	IVCCWECEK	9	PSA			21	3.11		0.041		
1.0269	QVHPQKVTK		PSA		 	182	3.11			0.019	
1.1112	SLYTKYVHYR	10	P5A		 				0.0000	0.014	
1.0653	LTAAHGRNK	10	PSA	·		237	3.11		0.28	0.23	
1.0651	RIVOGWECEK					57	3,11		0.14	0.083	
1.0662		10	PSA			20	3.11		0.046	0.067	
	KVVHYRKWIK	10	PSA .			241	3.11		0.045	0.045	
1.1111	VTKFMLCAGR	10	P5A			188	3.11		0.0003	0.012	
3.0108	MLURLSEPA	9 1	P5A			118	Random			- U.S. 1	

Table 23(K)

TABLE 24: CTL EPITOPES IDENTIFIED IN PEPTIDE SCHEENING.



		sitive	 borderline positive
1069.15	A03	нву	TLWKAGILYK
1069.01*	A01	нву	LLDTASALY*
1052.05	All	HCV	GVAGALVAFK
1069.62	A11	нсч	CTCGSSDLY
1073.10	A03	НСУ	GVAGALVAFK
1069.47	A11	HIV	VTVYYGVPVWK
1052.03	A11	HIV	TVYYGVPVWK
1069.56*	A03	НΙΥ	FLGKIWPSHK*
1069.46	A03	НΙΥ	WTYQIYQEPFK
966.01	A03	НΙΥ	AIFQSSMTK
1069.45	A03	HIV	KMIGGIGGFIK
1069.44	A03	HIV	KLAGRWPVK
1069.43	A03	HΙV	TVYYGVPVWK
1069.42*	•11/€V	AIH	<i>HARDVMATKAN</i>
1072,15	AII	MAGE1	ESLFRAVITK
1072.39	A11	MAGEIN	RALAETSYVK
1072.13	119	MAGE1	SLFRAVITK
1072.38*	A03	MAGEIN	ALAETSYVK*
1072.03+	A01	MAGE3	GSVVGNWQY *
1072.02*	A01	MAGE3	SSLPTTMNY *
958.01	A01	MAGE1	EADPTGHSY
1044.01	A01	MAGE3	ASSLPTTMNY
1044.07	A01	MAGE3	EVDPIGHLY
Jd	Motif	Antigen	S qu nc





Table 25 a

Peptides Synthesized by Cytel For Loading Onto Acid Stripped Autologous PBMCs and PHA Blasts

	Peptide ID #	Antigen	Sequence
	777.03	HBs	FLLTRILTI
10	924.07	НВс	FLPSDFFPSV
	927.32	HBp	GLYSSTVPV
	938.01	MAGE 1	EADPTGHSY
	939.03	PSA	VLVHPQWVL
	941.01	нвс	FLPSDYFPSV
15	1044.04	PAP	ILLWDPIPV
	1044.05	PSA	KLQCVDLVHI
	1044.06	PSA	MLLRLSEPAEL

20	Table 25 b			
	Cell Population	125I-Labeled	CPMS	
		Peptide +/- Cold	+/- std. dev.	
		Peptide		
	JY acid stripped	 cold peptide 	3553 ± 157	n = 3
25	JY acid stripped	+ cold peptide	13	n = 1
	JY control	-cold peptide	370 ± 37	n = 3
	JY control	+ cold peptide	50	n = 1